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FIGURE 1

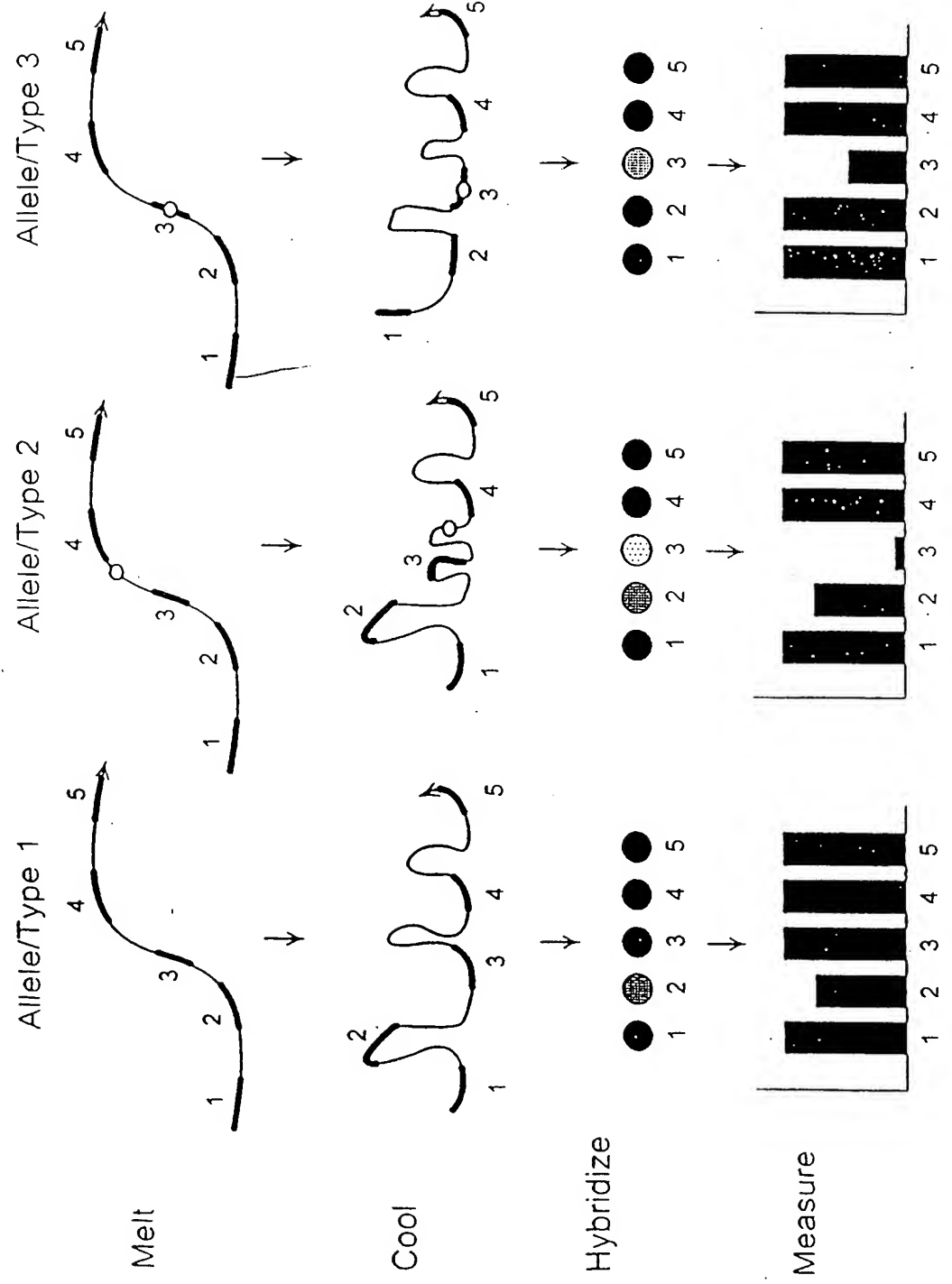


FIGURE 2

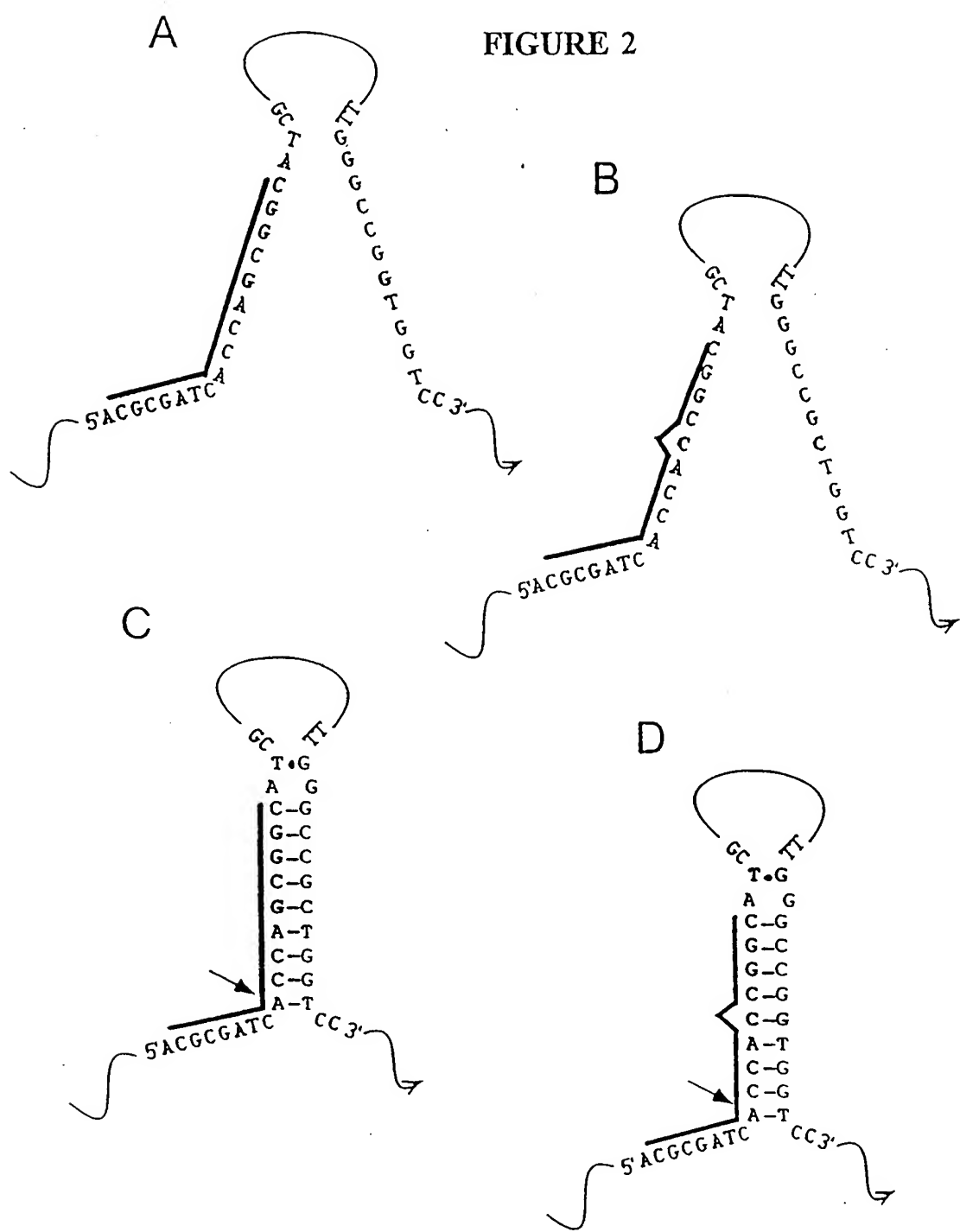


FIGURE 3

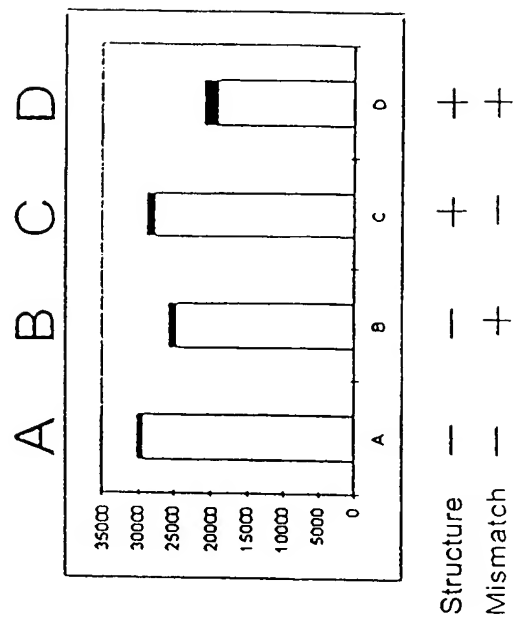
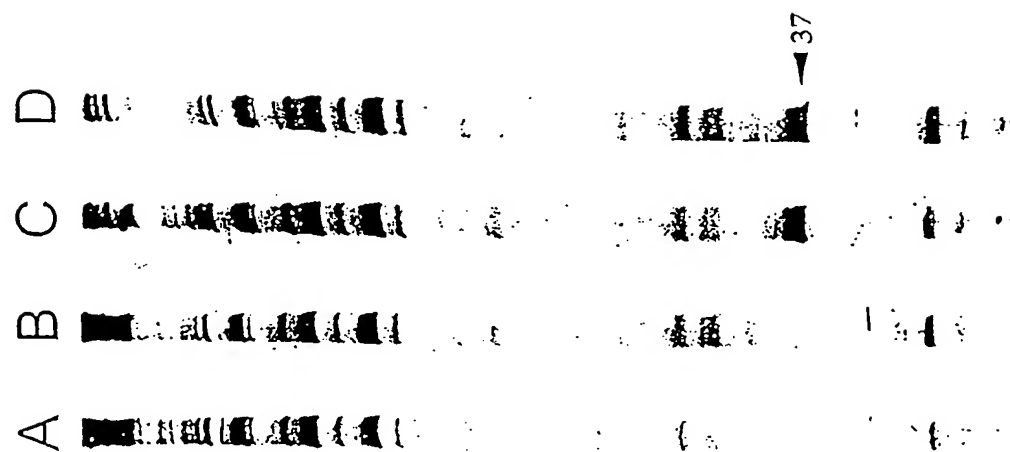


FIGURE 4

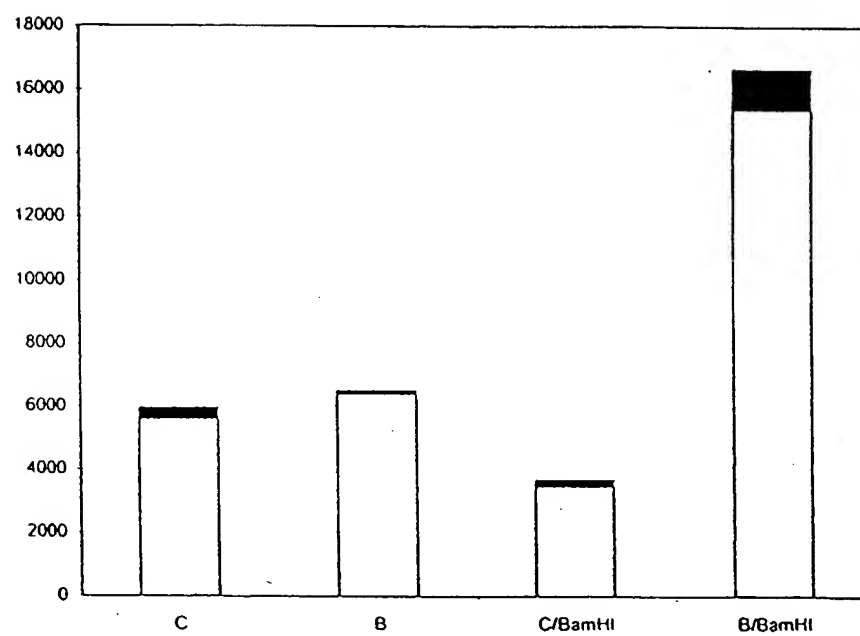


FIGURE 5

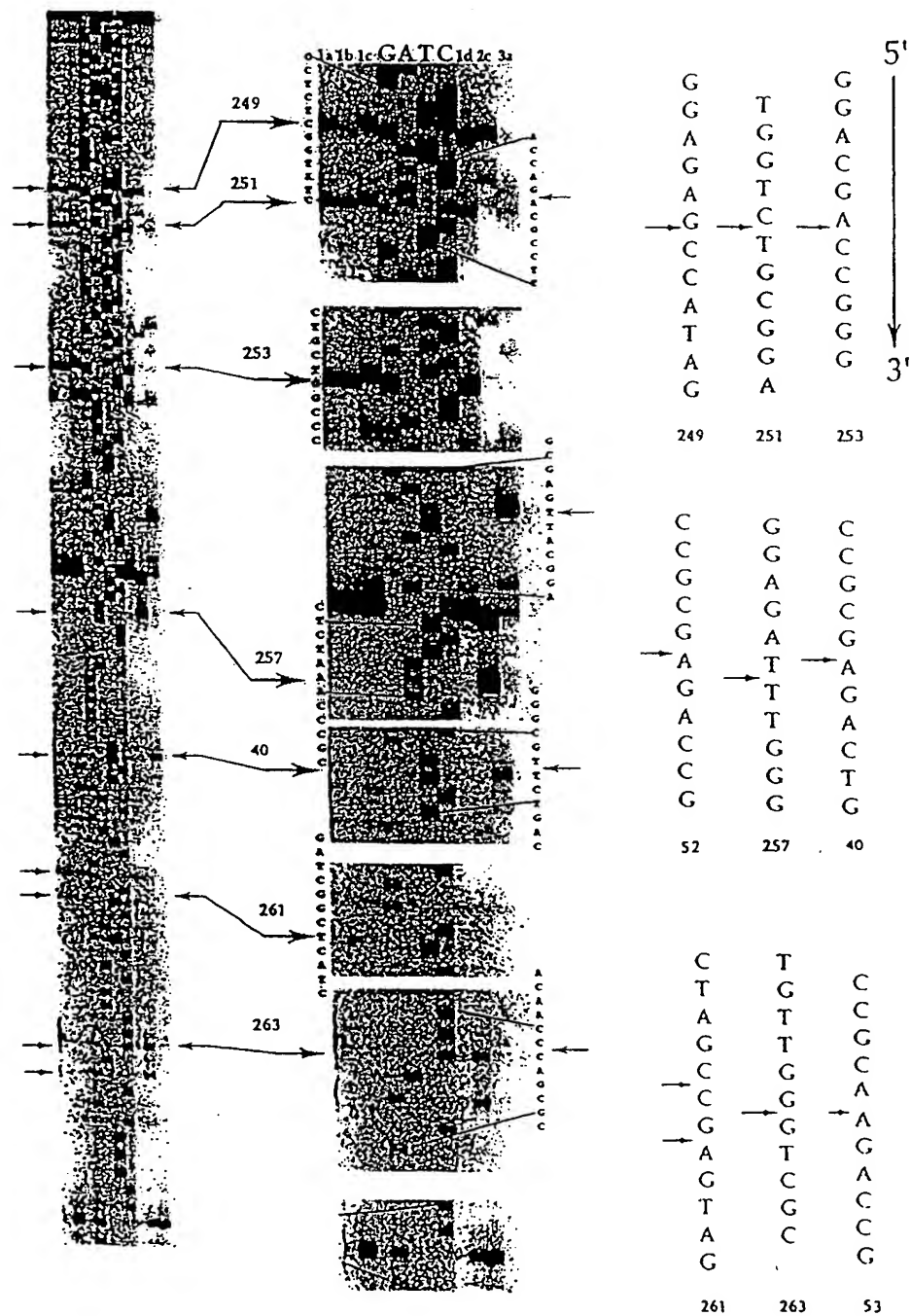


FIGURE 6

Consensus:	GATTCTGTCT	TCACGCAGAA	AGCGTCTAGC	CATGGCGTTA	GTATGAGTGT	CGTGCAGCCT
HCV 1a	-----	-----	-----	-----	-----	-----
HCV 1b	-----	-----	-----	-----	-----	-----
HCV 2c	-----	-----	-----	-----	-----	-A-----
HCV 3a	-----	-----	-C-----	-----	-C-----	-----

	#249	#251
CCAGGACCCC	<u>CCCTCCCCGG AGAGCCATAG</u>	<u>TGGTCTGCGG AACCGGTGAG</u> TACACCGGAA
-----	-----	-----
-T-----	-----	-----
-C-----	-----	-----
-----	-A-----	-----

	#253	#257
TTGCCAGGAC	<u>GACCGGGTCC</u> TTTCTTGGAT	CAACCCGCTC <u>AATGCCCTGGA</u> GATTGGGCG
-----	-----	-----
-----	-----	-----
-G--A	-T-----	A--A--T--C-C
-C-TG-GT	-----	-G-----A-CA-A

	#40	#261	#263
TGCCCCCGCA	<u>AGACTGCTAG</u> CCGAGTAGTG	<u>TTGGGTGCGG</u> AAAGGCCTTG	TGGTACTGCC
-----	-----	-----	-----
-G-----	-----	-----	-----
-----	-----	-C-----T	-----
-G-----	-TCA-----	-----	-----

TGATAGGGTG	CTTGCGAGTG	CCCCGGGAGG	TCTCGTAGAC	CGTGCAATC
-----	-----	-----	-----	-----
-----	-----	-----	-----	-----
-----	-A-----	-----	-----	-----
-----	-----	-----	-----	-----

FIGURE 7

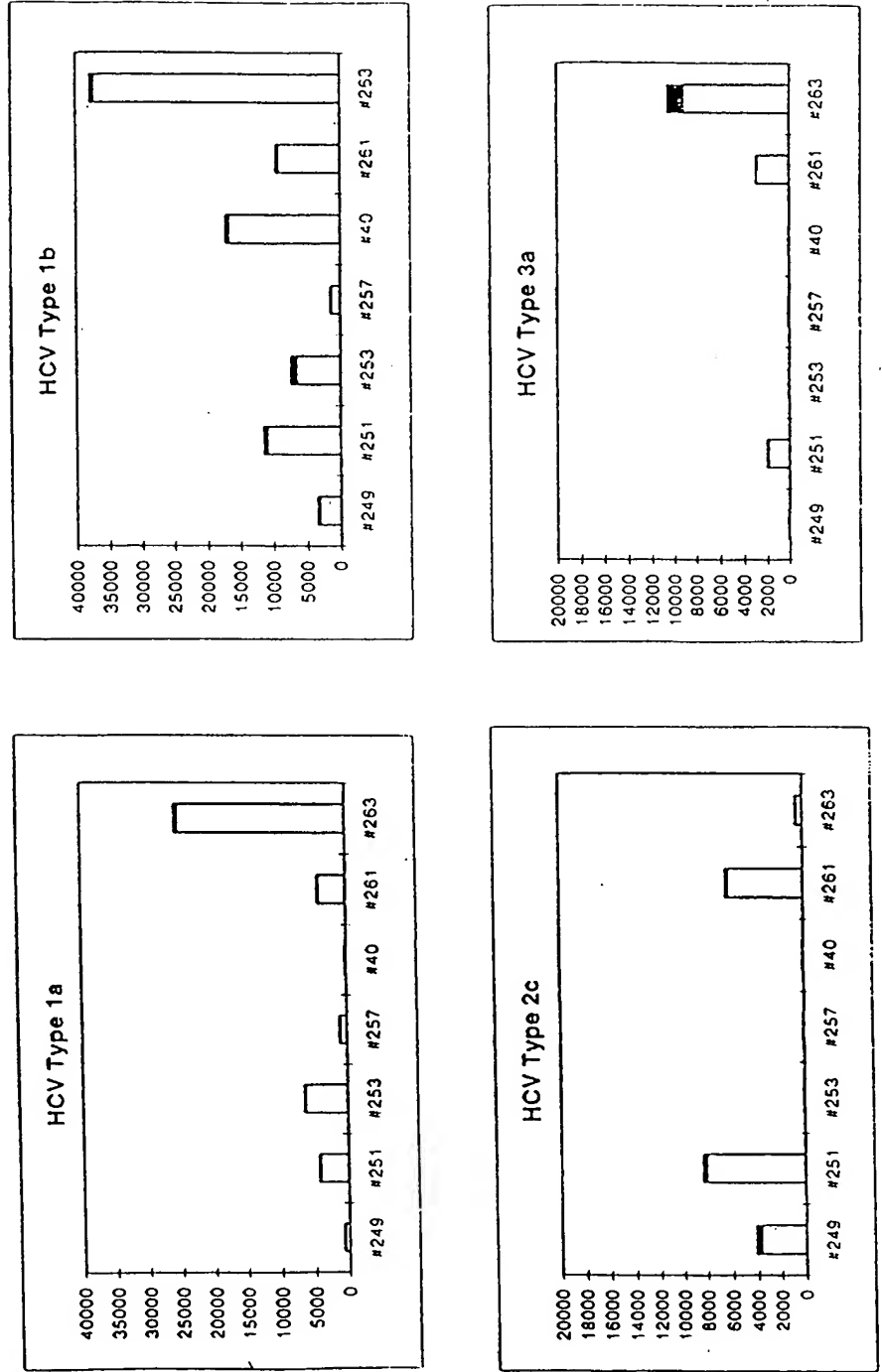




FIGURE 8A

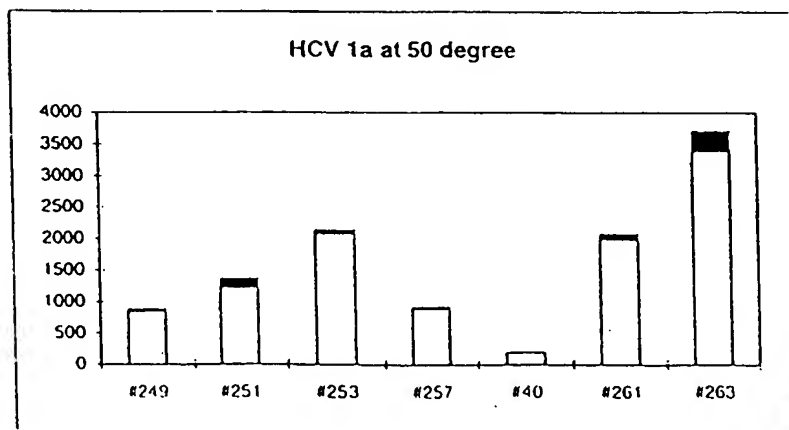
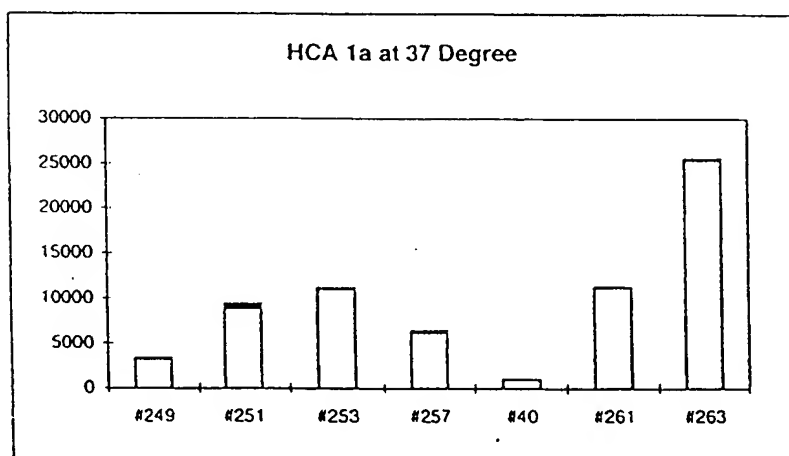
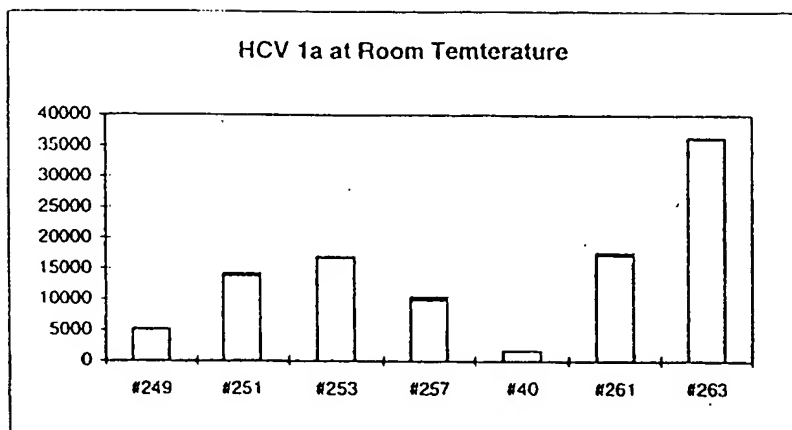


FIGURE 8B

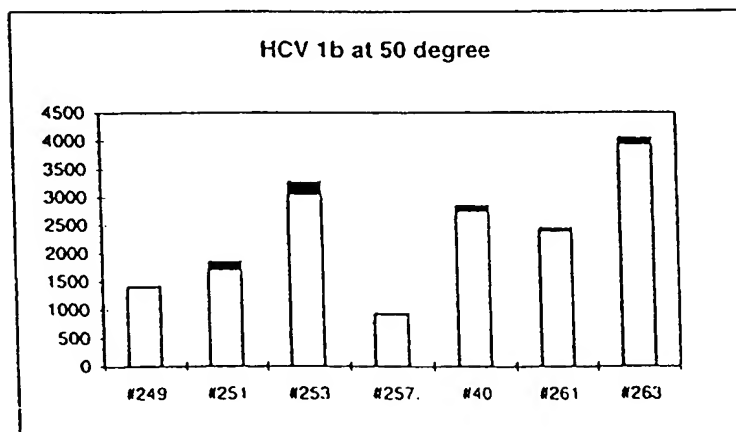
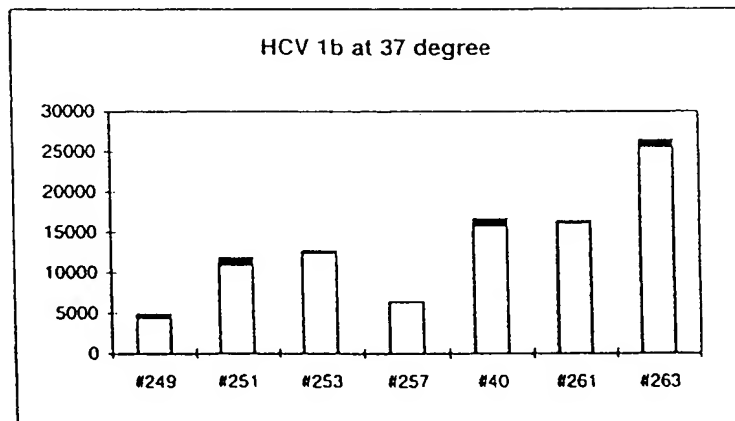
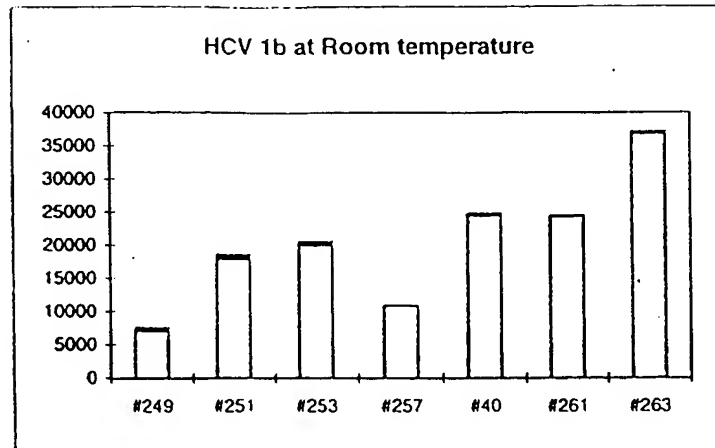


FIGURE 8C

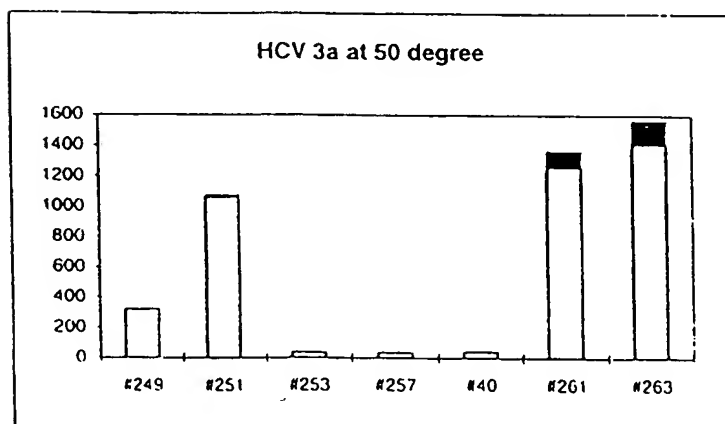
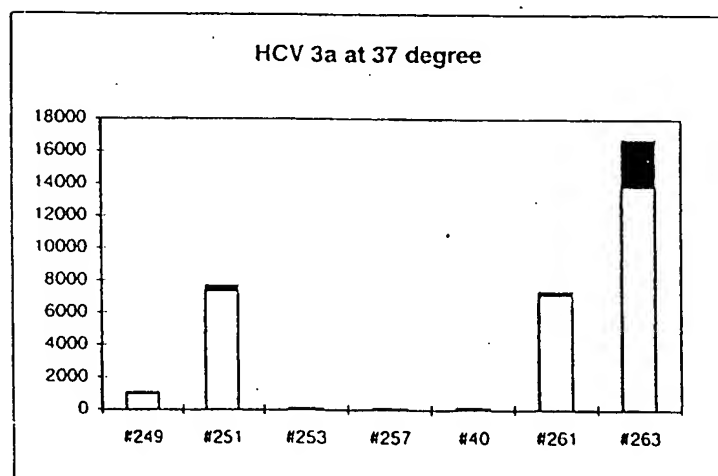
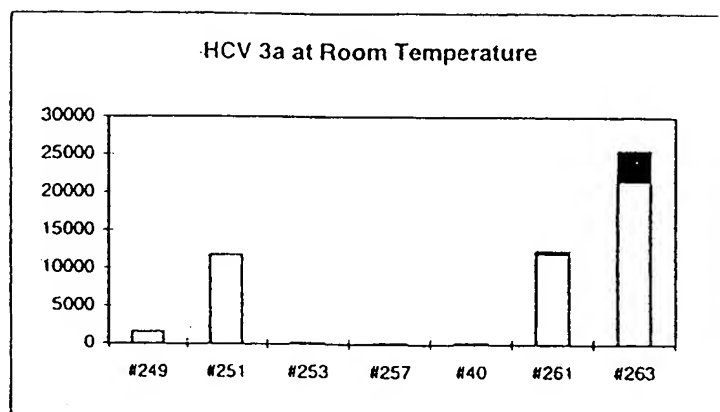


FIGURE 9A

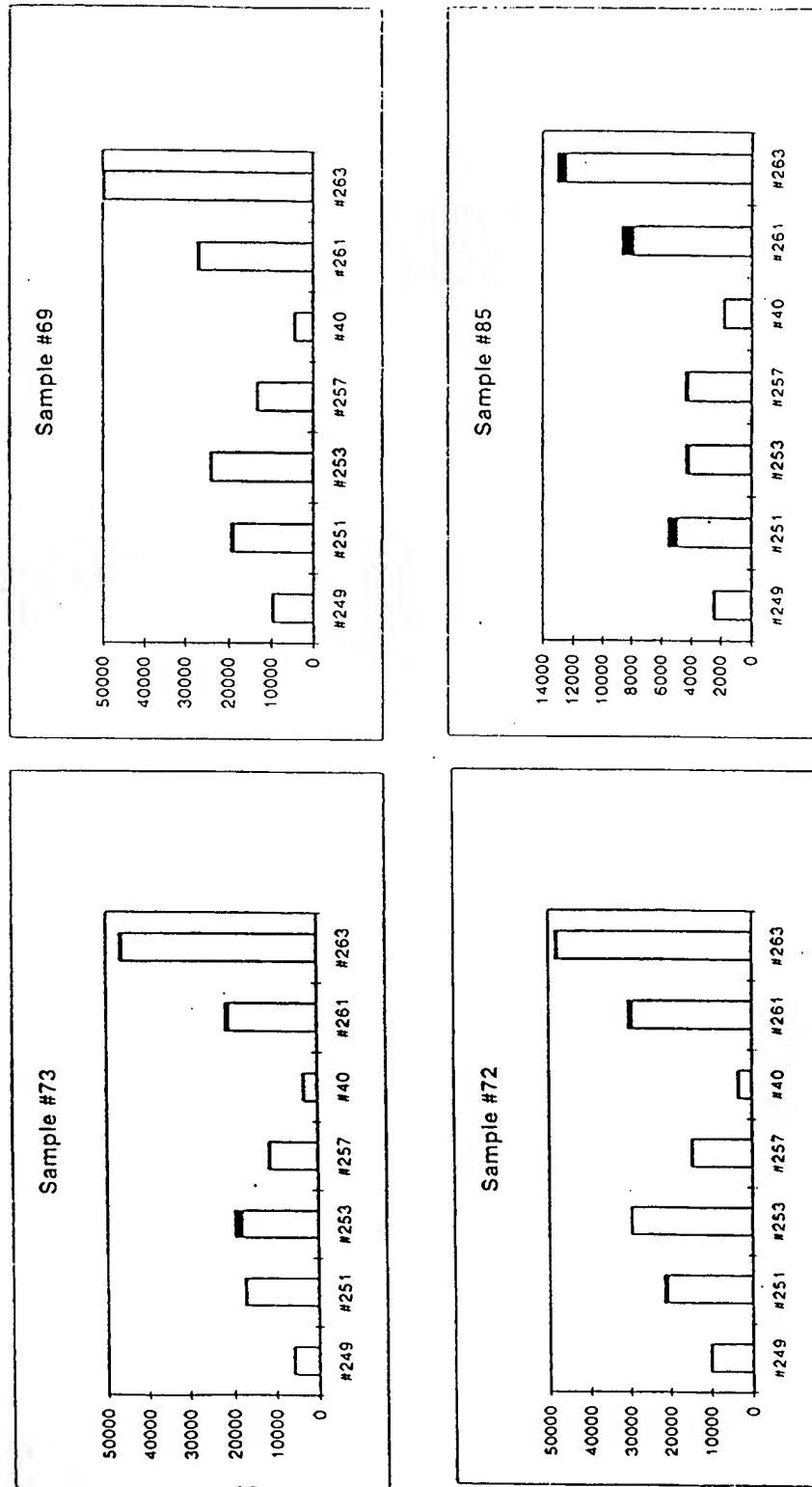


FIGURE 9B

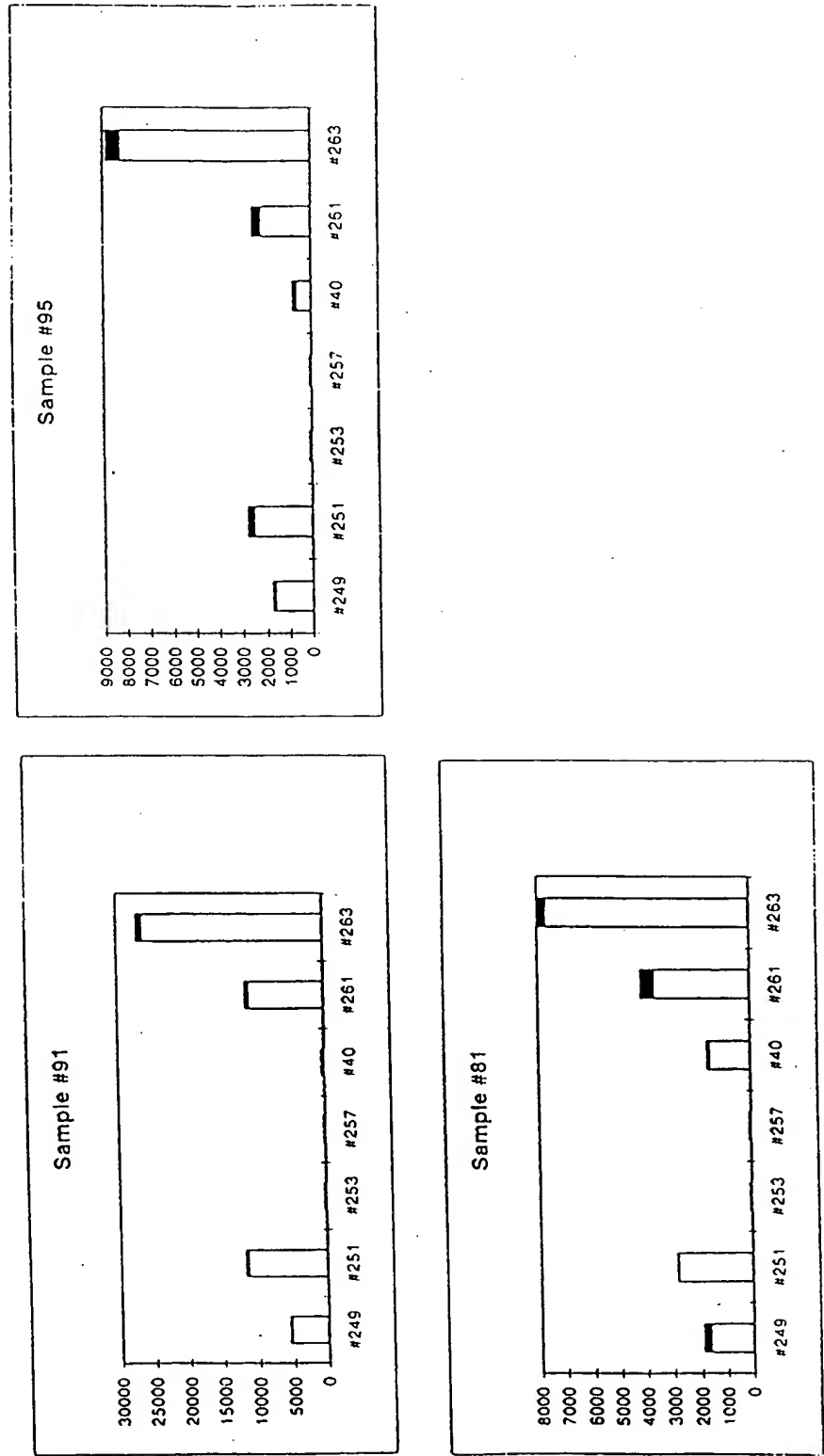


FIGURE 9C

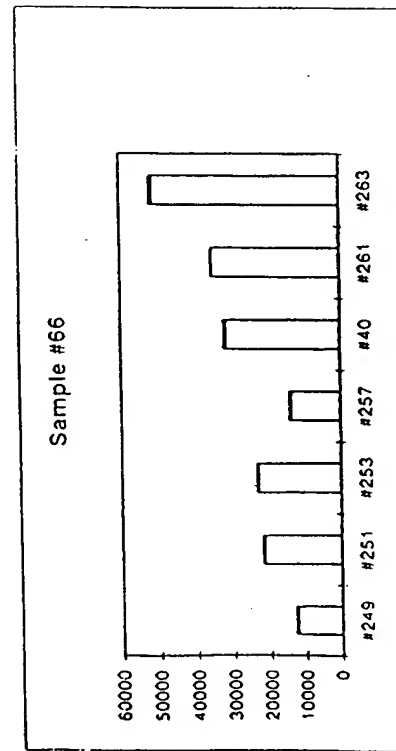
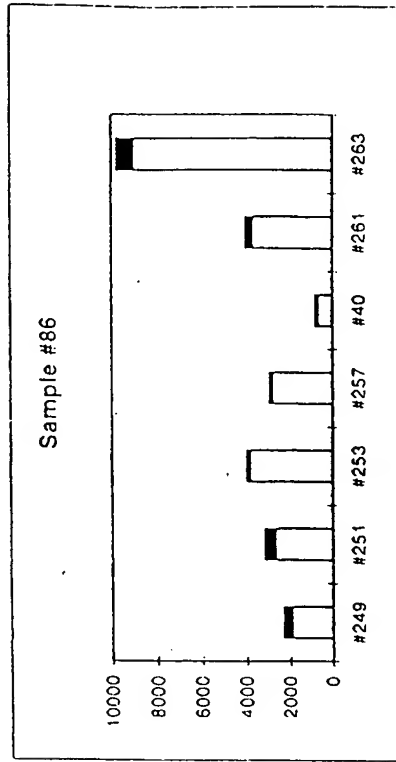


FIGURE 9D

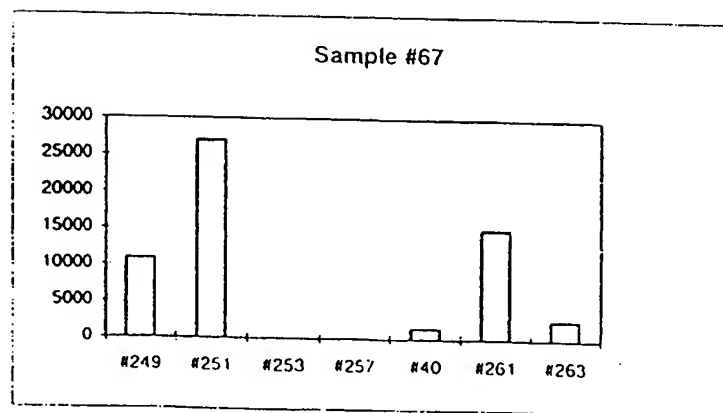
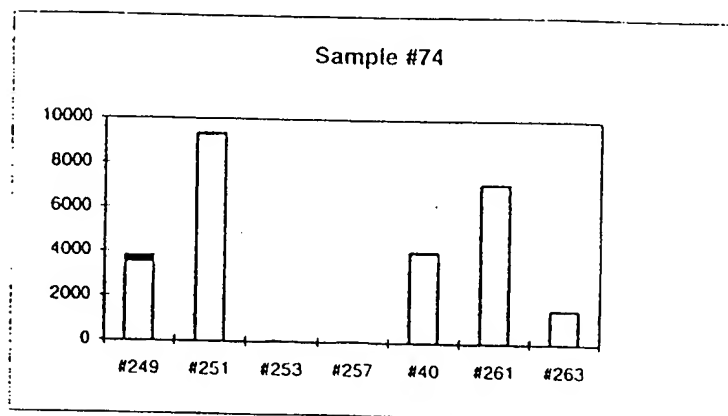


FIGURE 10

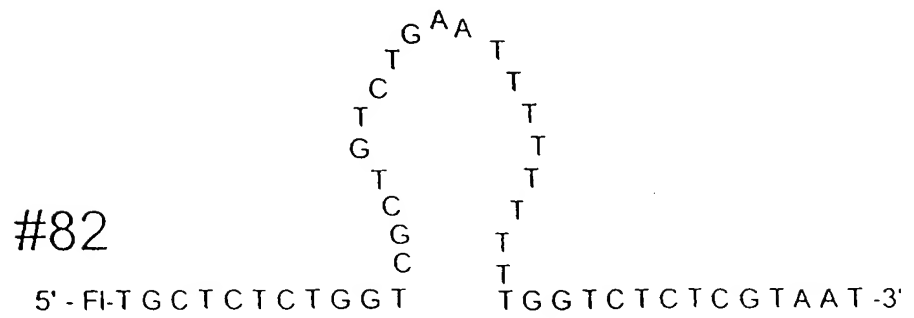
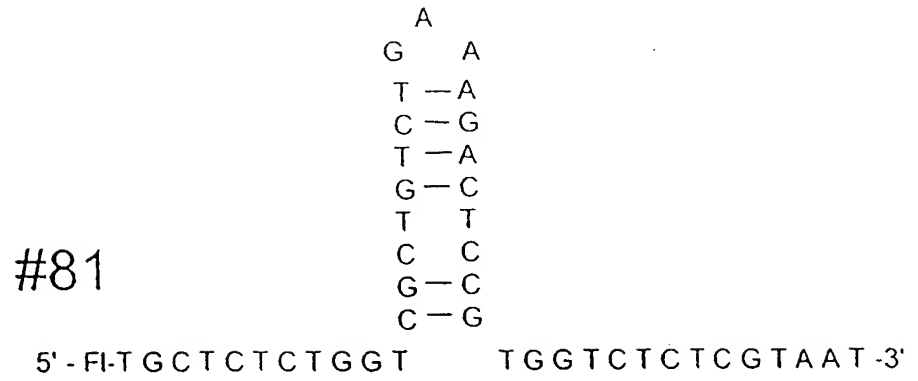
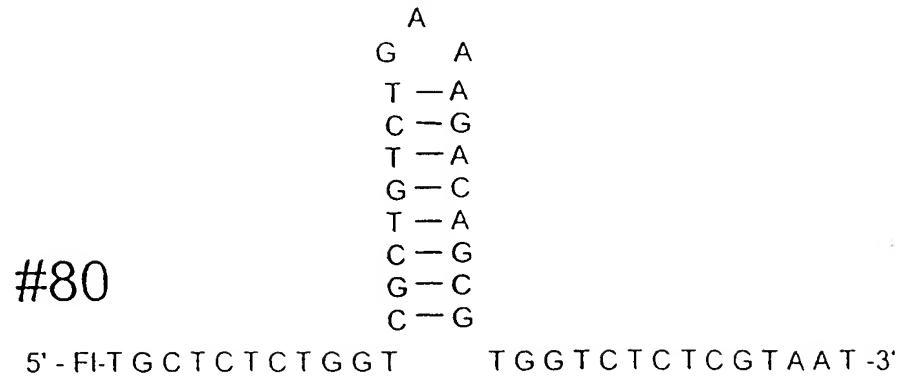




FIGURE 11A

#2) 5' Biotin

```

      I
      T   A
    C   G   A
    A   T - A
    G   C - G
    A   T - A
    C   G - C
    A   T - A
    G   C - G
    C   G - C
    G   C - G
  
```

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#91) 3' Biotin - CGAGAGACCA-5'

```

      A
    G   A
    T - A
    C - G
    T - A
    G - C
    T - A
    C - G
    G - C
    C - G
  
```

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#78) 3' - AGACCATTACCAGA -Biotin 5'

#4) 3' - GAGACCATTACCAGAG -Biotin 5'

#79) 3' - AGAGACCATTACCAGAGA -Biotin 5'

↓ ↓

#116) 3' - AGAGACCAACCAGAGA -Biotin 5'

#117) 3' - TACCAGAGA -Biotin 5'

#118) 3' - AGAGACCAT - 5'

FIGURE 11B

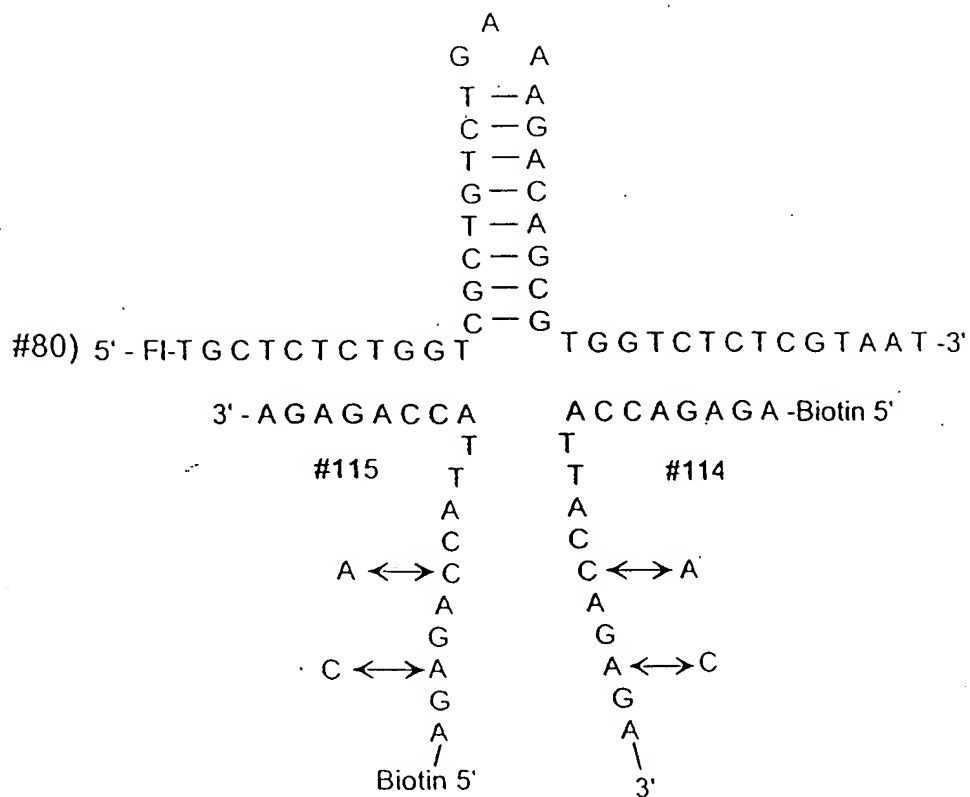
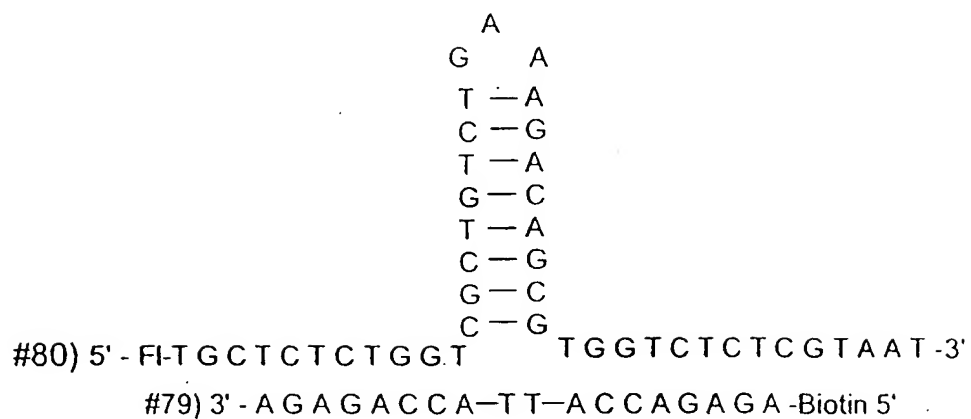
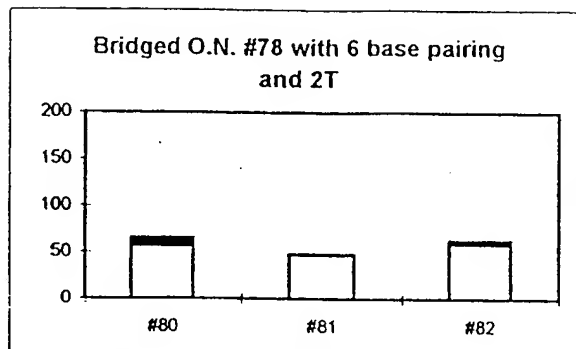
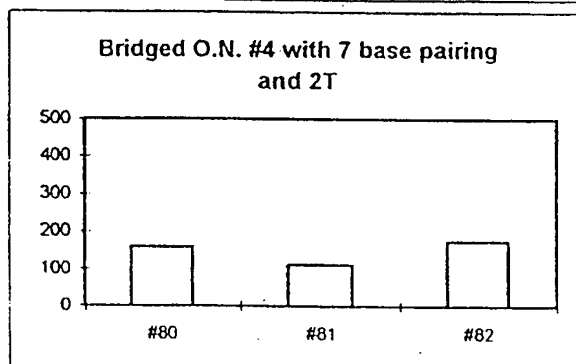


FIGURE 12

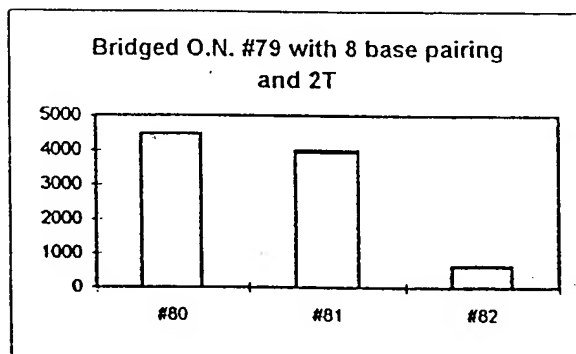
A



B



C



D

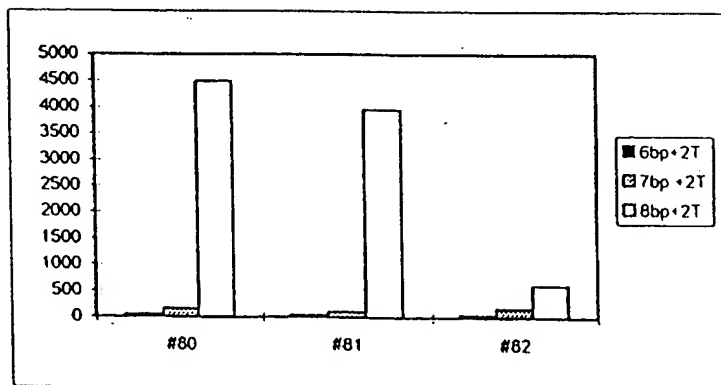


FIGURE 13A

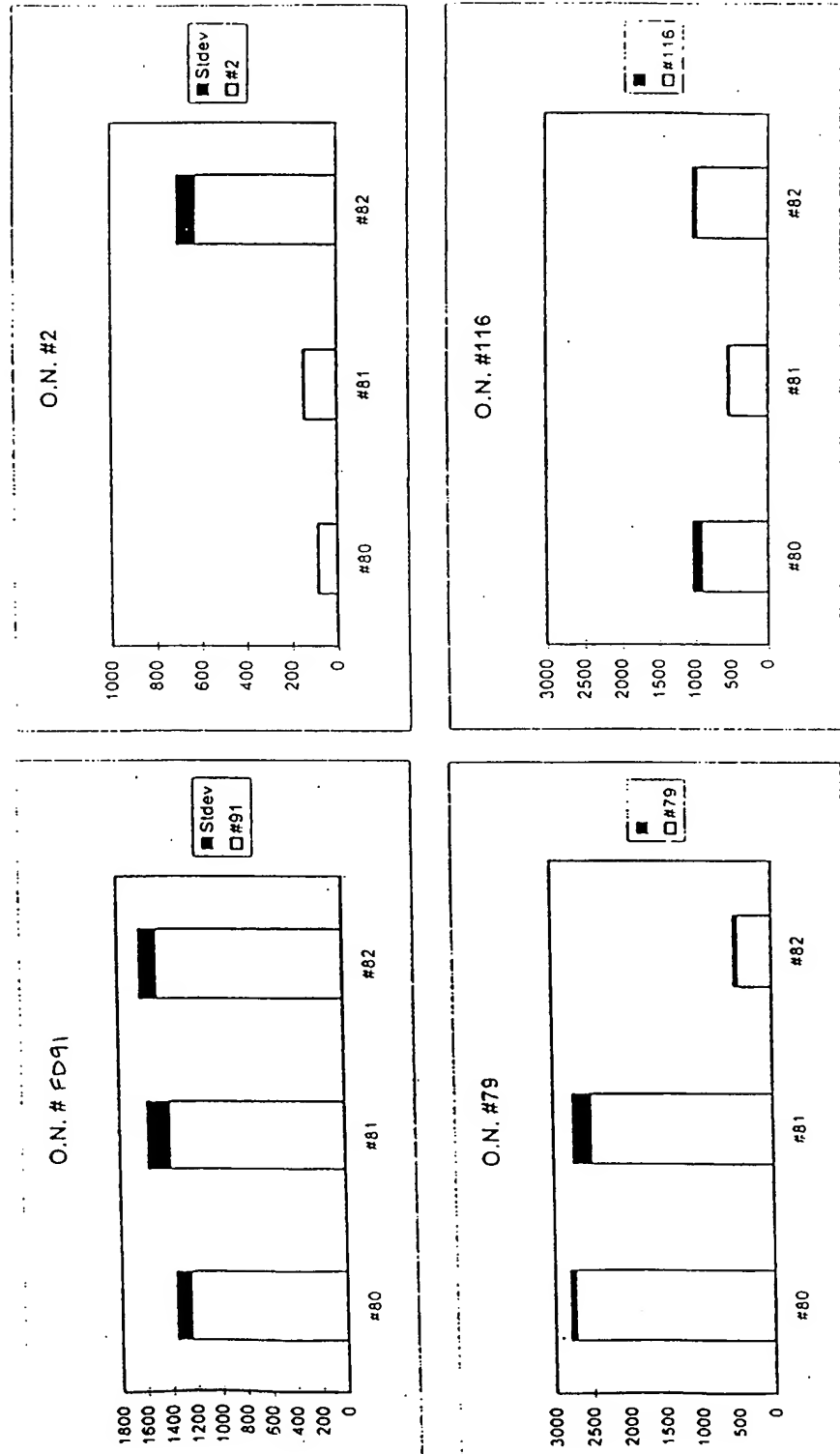


FIGURE 13B

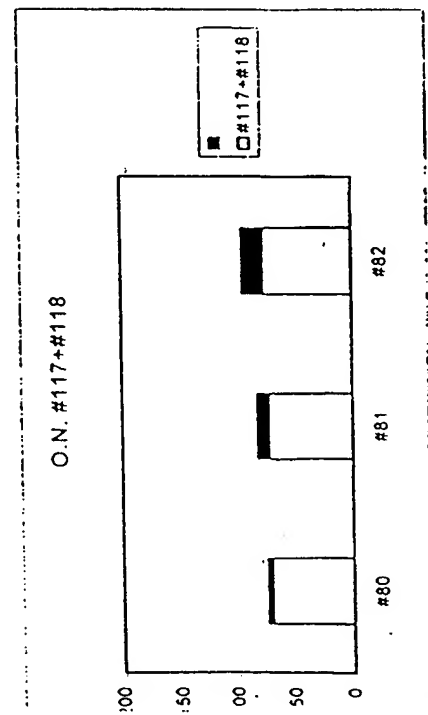
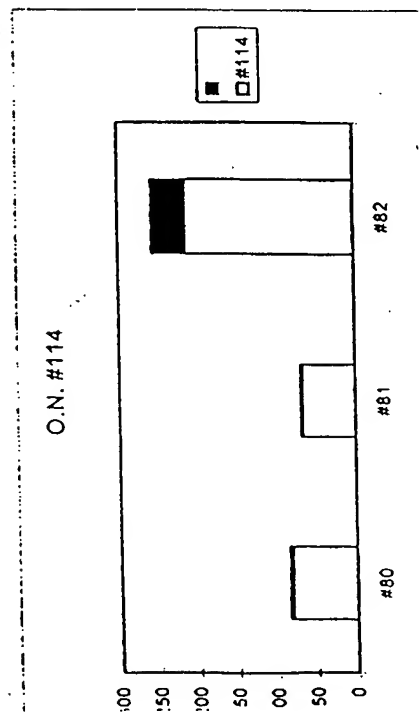
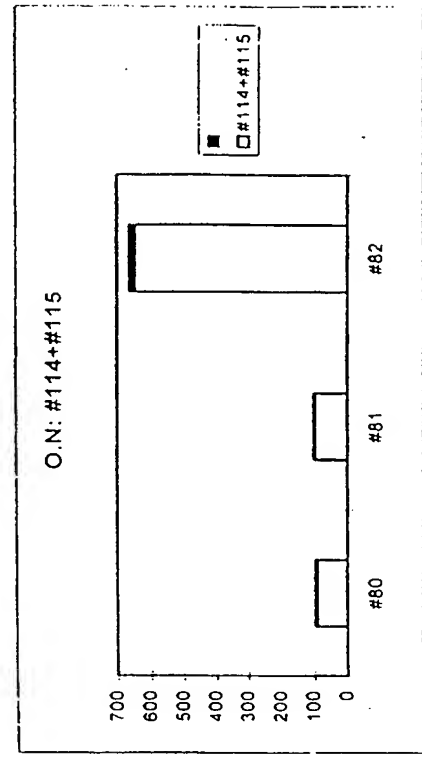
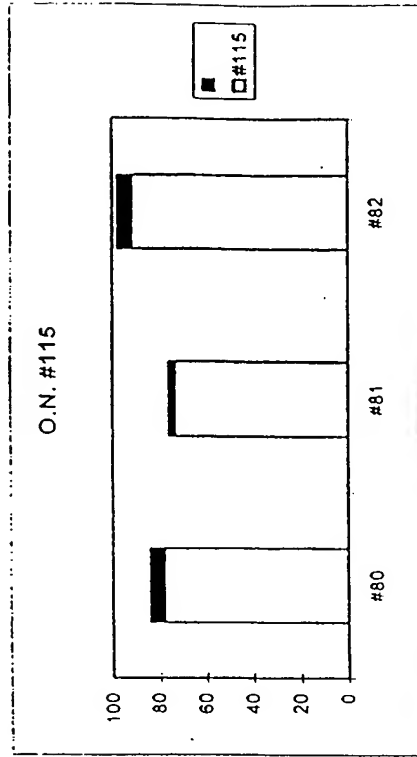


FIGURE 14

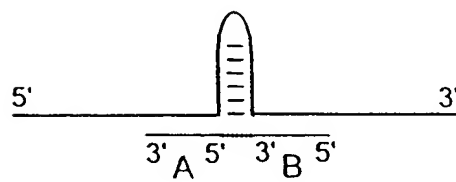
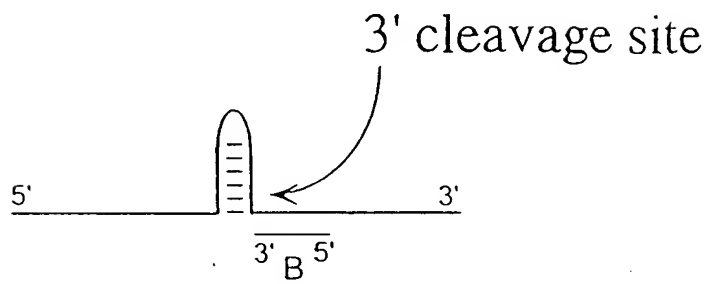
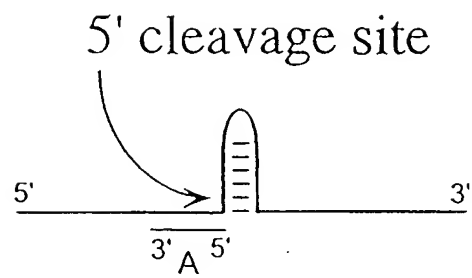


FIGURE 15

[illegible]

FIGURE 16A

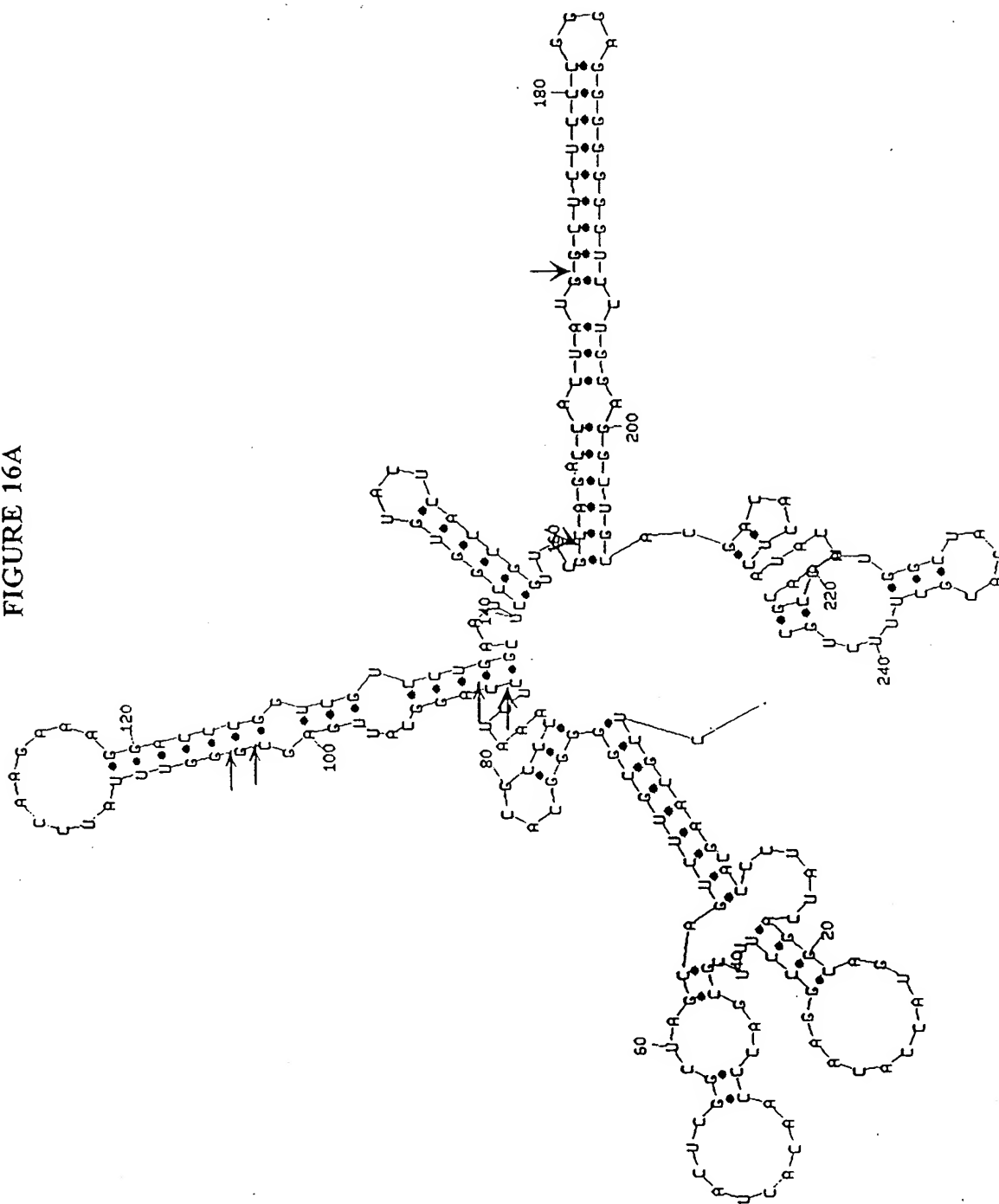




FIGURE 16B

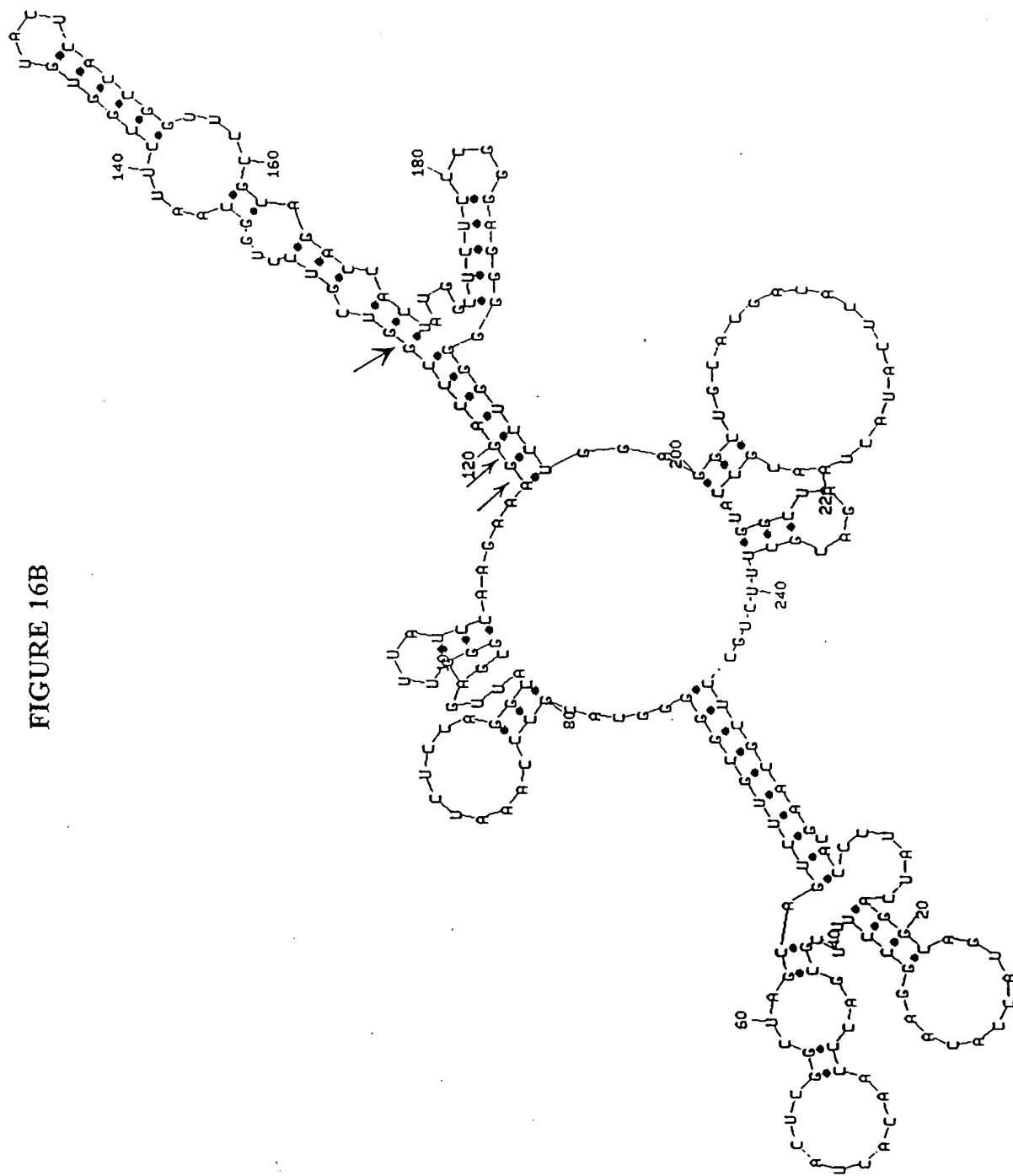
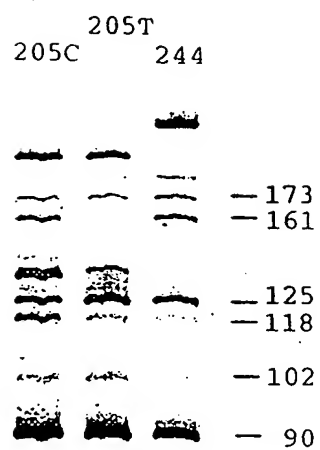


FIGURE 17A





5' Biotin—AAATCT 141CG<sup>156161</sup>GC<sup>205</sup>ACGACACT—3'  
 (179-49-01)3'—GGCCAAGGTTTGCTGTGA—Fl-5'  
 (#81-01)3'—TTAA<sup>TT</sup>AAGG<sup>TT</sup>TGCTGTGA—Fl-5'

5' Biotin — TCCAAGAA GGAGGCTG — 3'

m (#81-04) 3'—AGGTTCTT CC CCTCCGAC—Fl-5'

FIGURE 18A

# HCV 1a

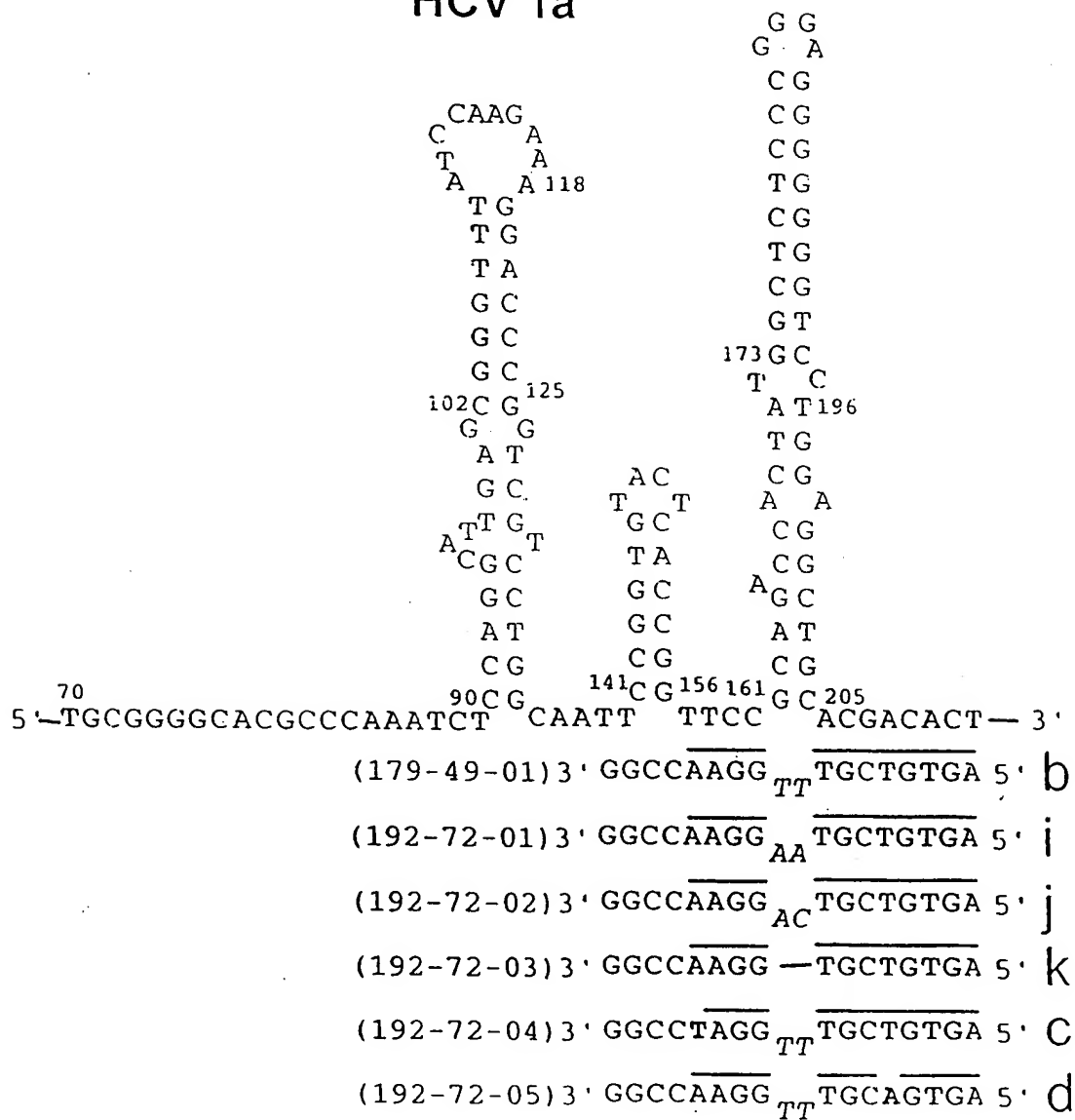


FIGURE 18B

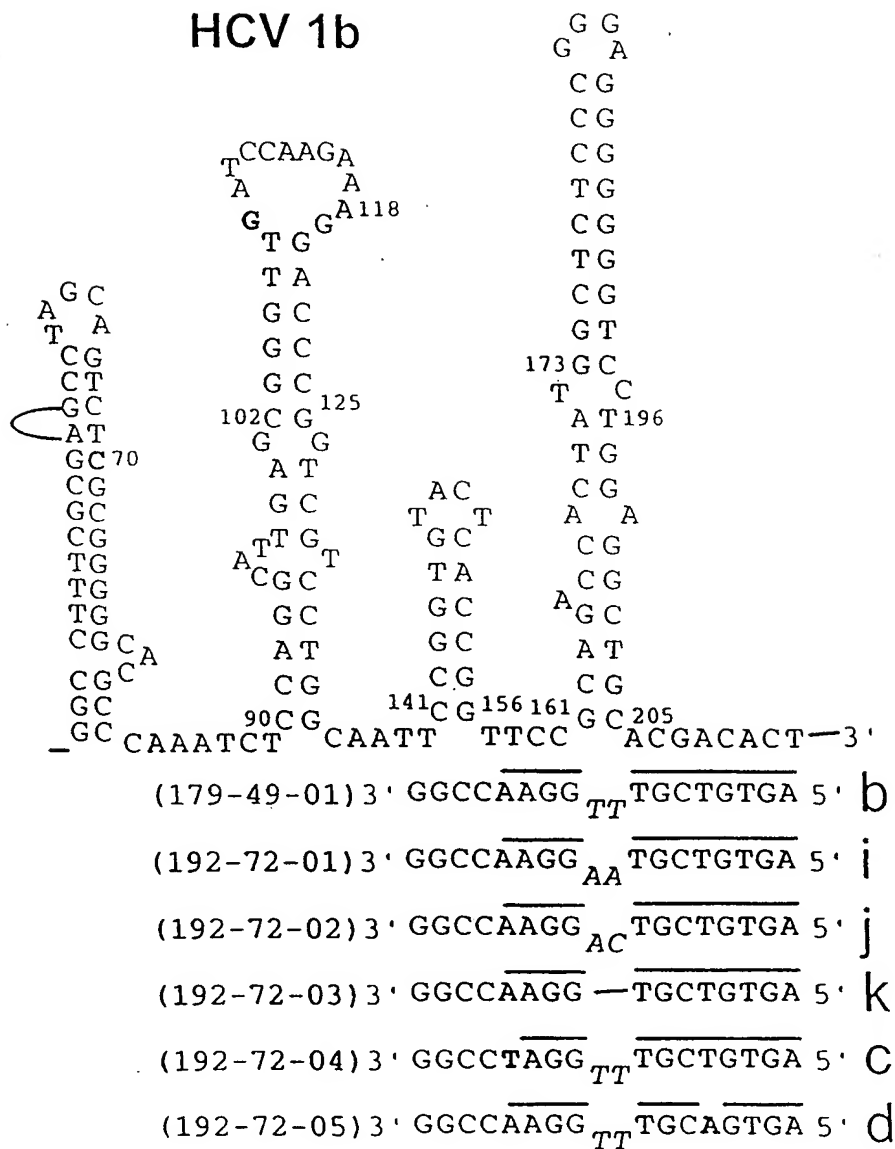


FIGURE 18C

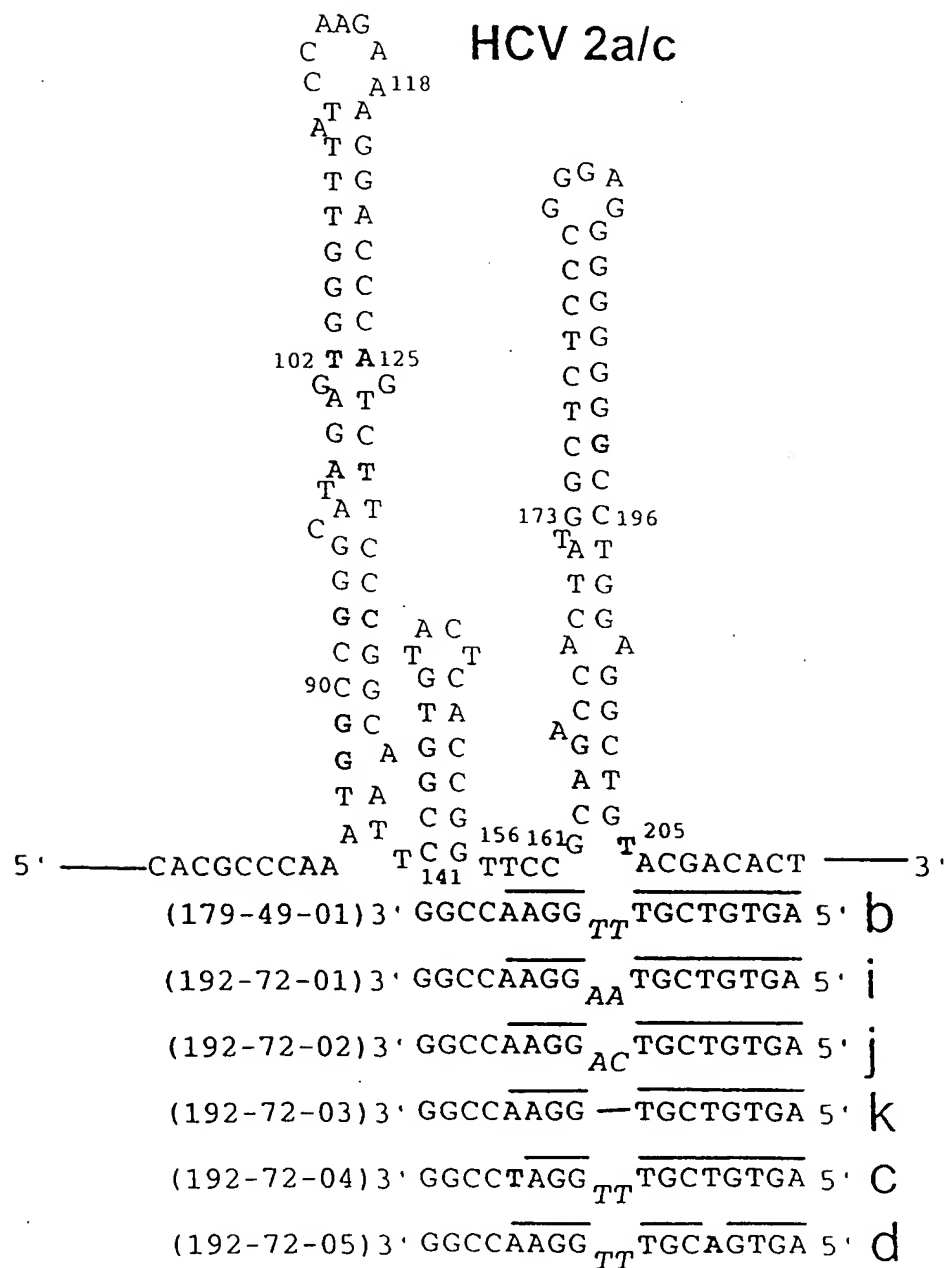


FIGURE 18D

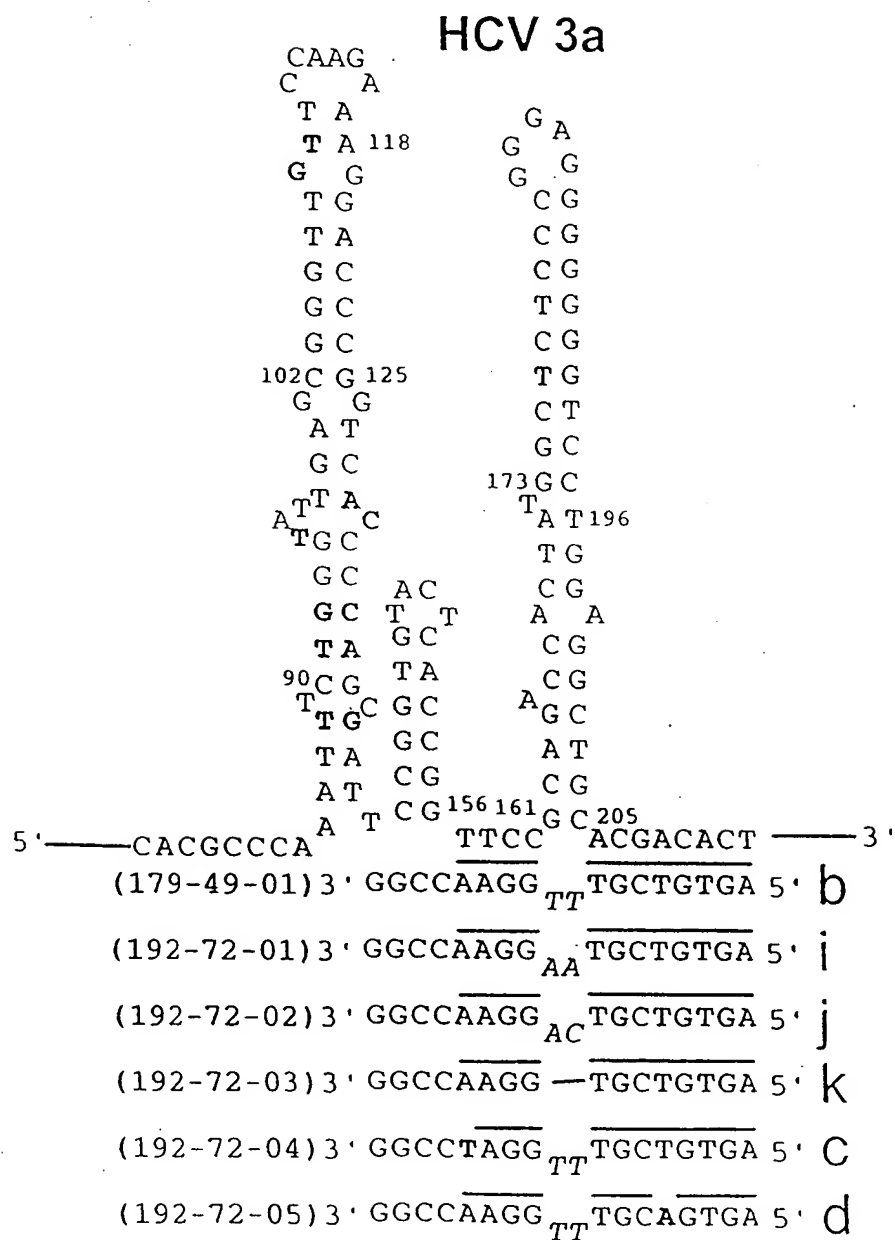




FIGURE 19

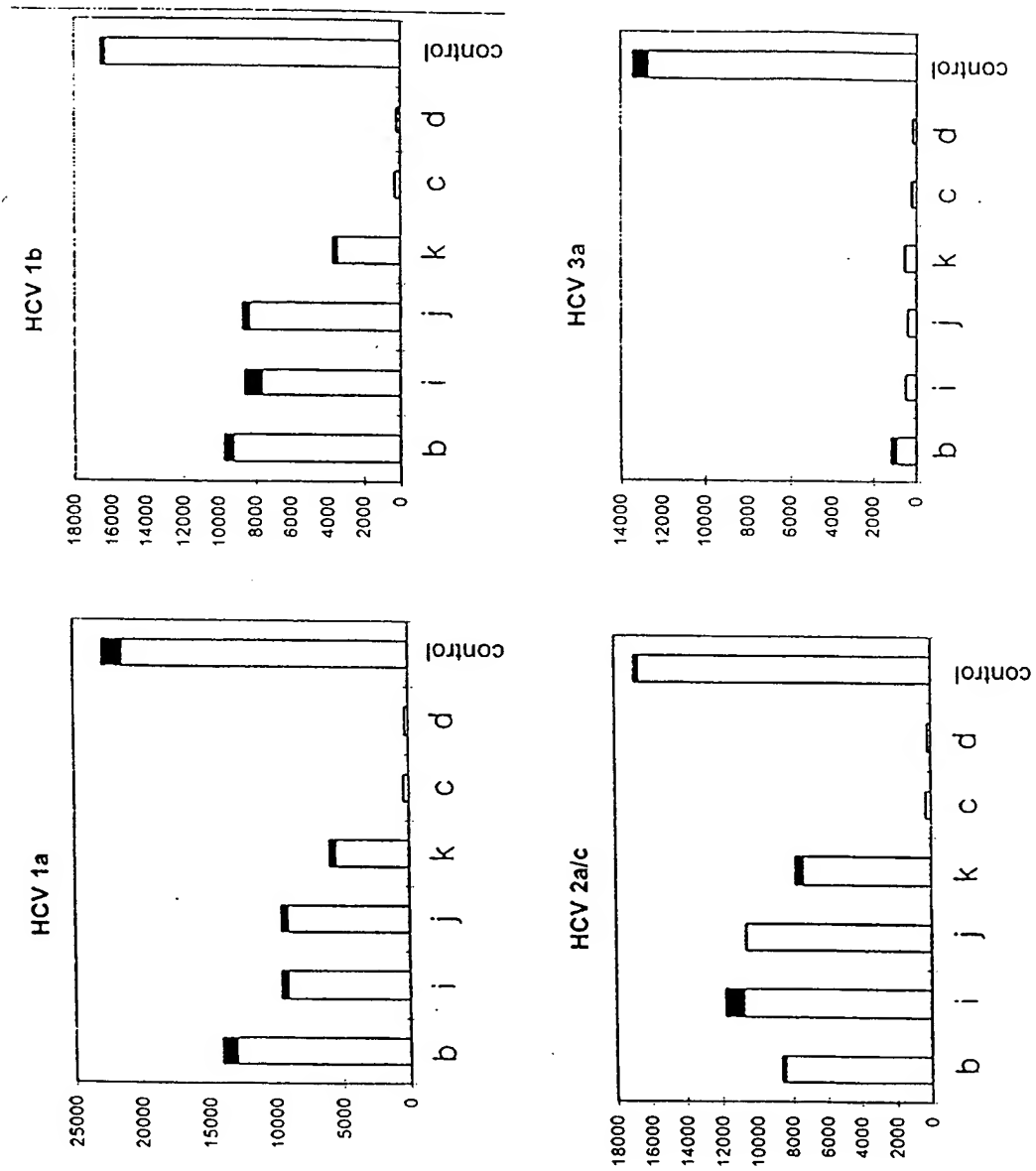
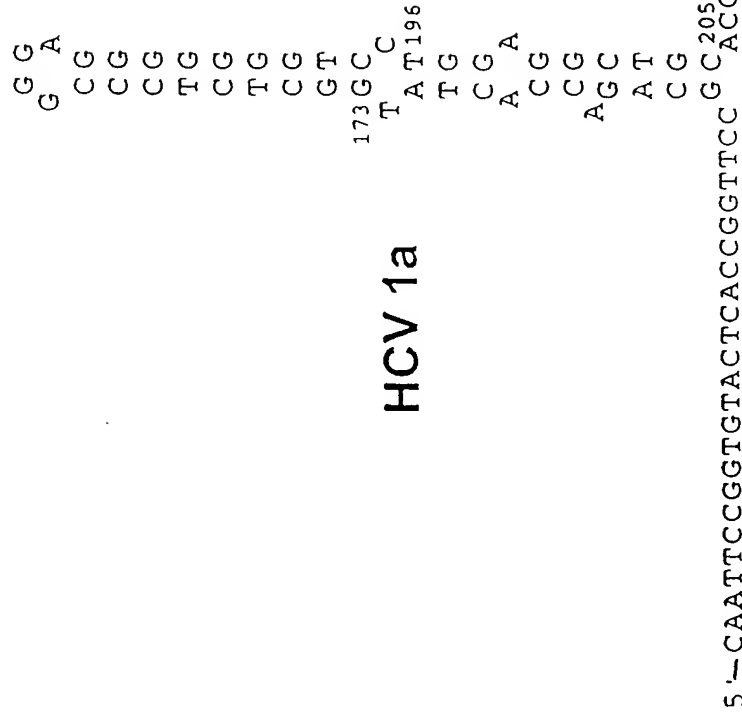


FIGURE 20A



- 3'-GGCCAAAGGCGTCTGGTGA-F1'5' (205-13-02) a
- 3'-GGCCAAAGG<sub>TT</sub>TGCTGTGA-F1'5' (179-49-01) b
- 3'-GGCCCTAGG<sub>TT</sub>TGCTGTGA-F1'5' (192-72-04) c
- 3'-GGCCAAAGG<sub>TT</sub>TGCAGTGA F1'5' (192-72-05) d
- 3'-GGCCAAAGG-F15' (205-27-01) e

FIGURE 20B

HCV 1a

5'-CAATTCGGGTGTA<sup>CT</sup>CA<sup>CC</sup>GGTTC<sup>3'</sup>  
 3'-GGCCAAGG<sup>5'</sup>  
 (205-13-02) a



FIGURE 22

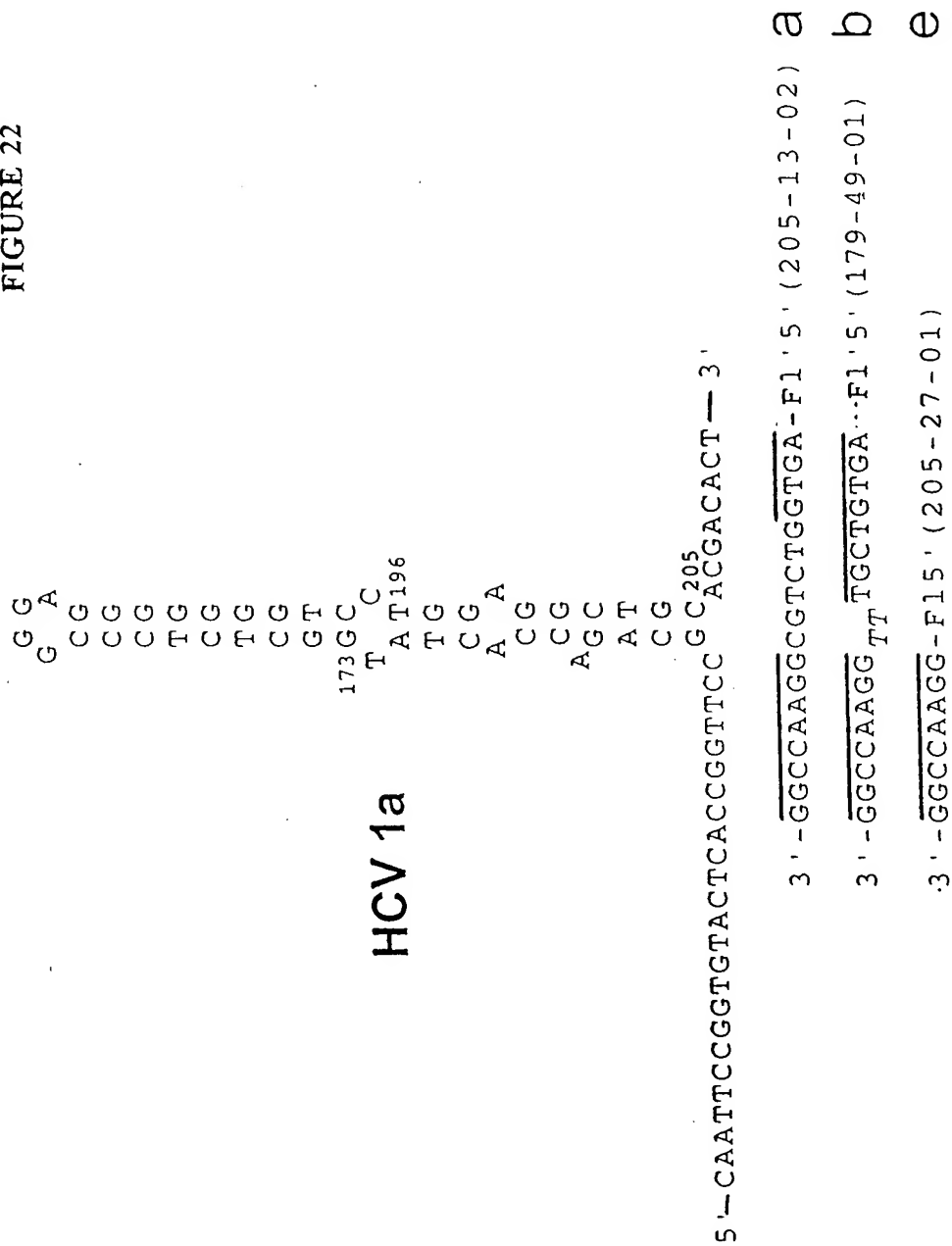


FIGURE 23

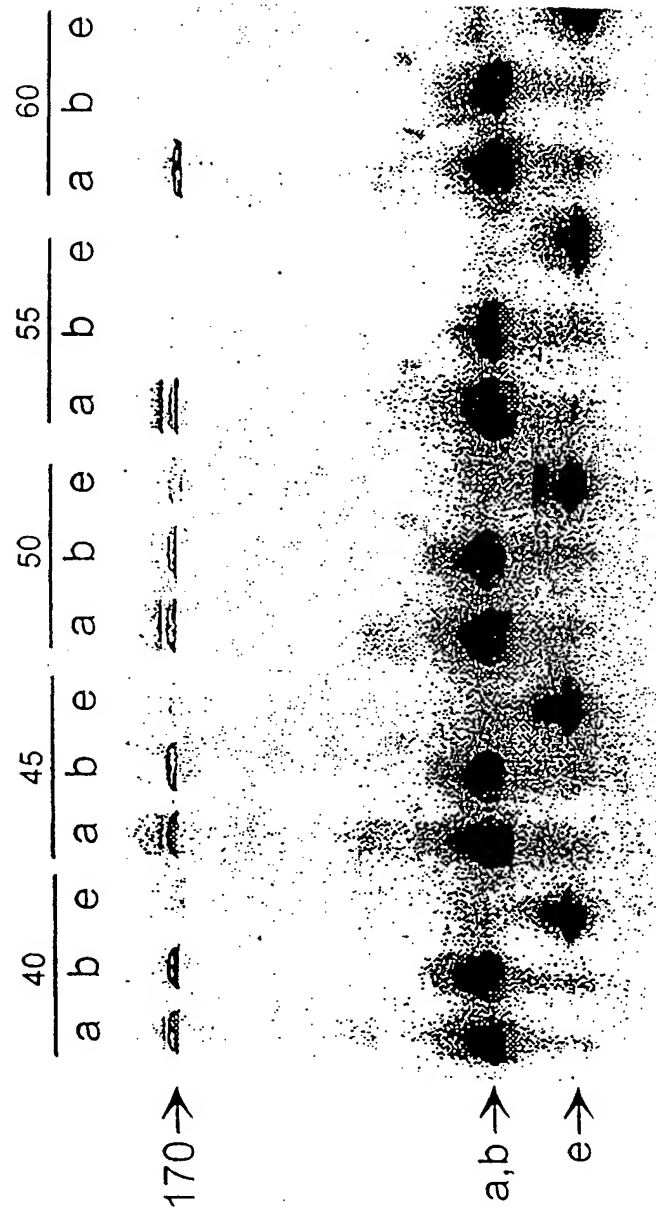


FIGURE 24

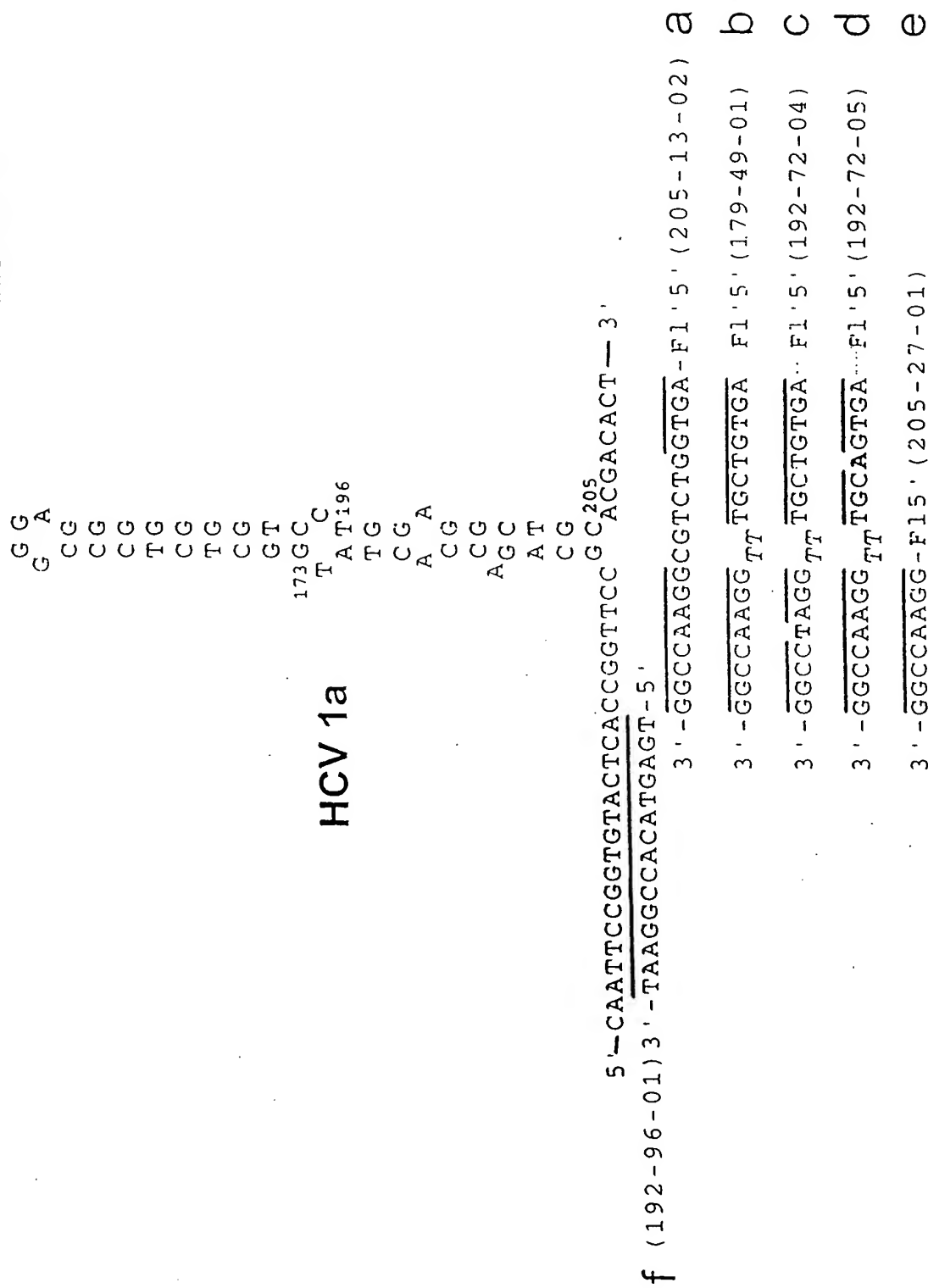


FIGURE 25

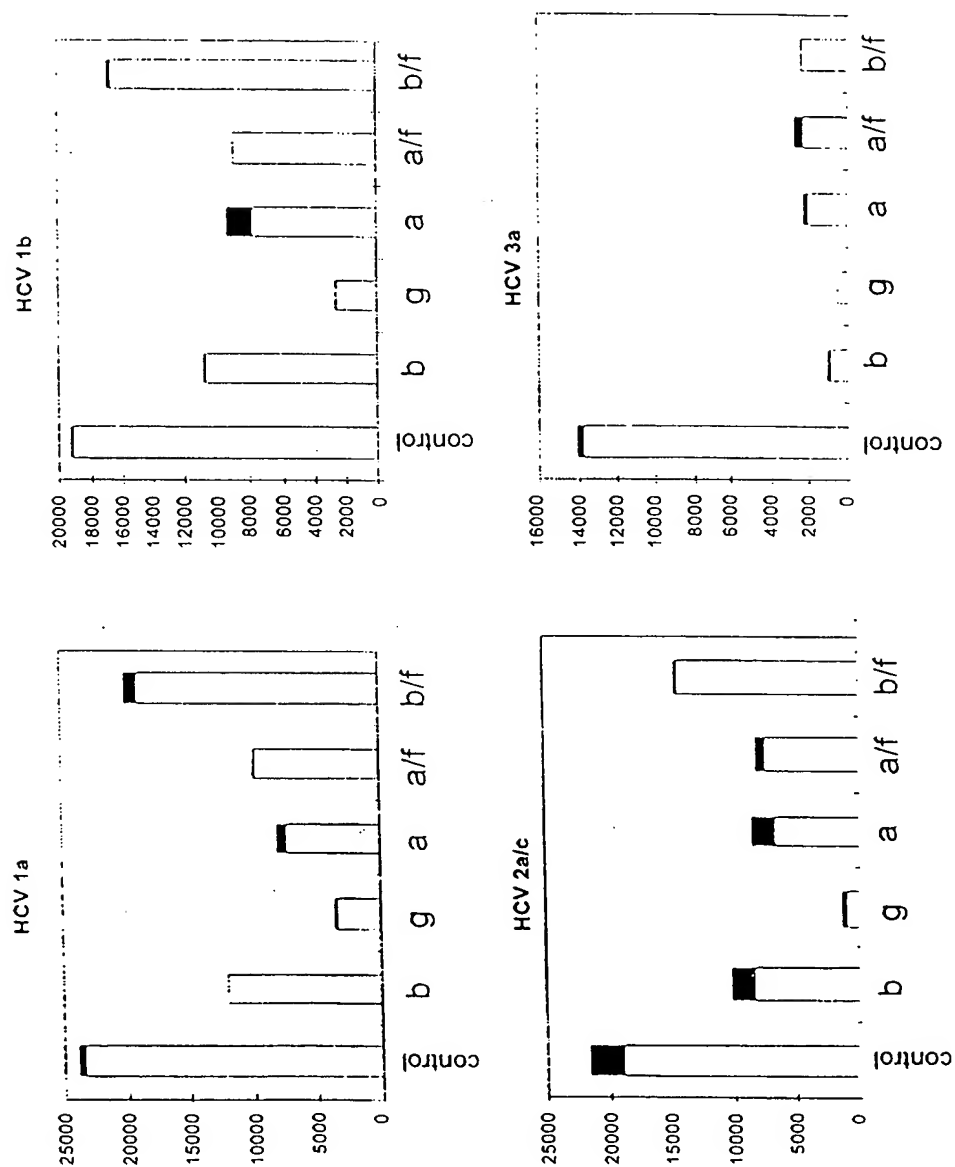




FIGURE 26

5' -ATTCCGGTGTACTCACCGGTTCCAAACGACACT-3' (205-13-01) S.T.  
 f (192-96-01) 3' -TAAGGCCACATGAGT-5'  
 3' -GGCCAAAGCGCTCTGGTGA-F1'5' (205-13-02) a  
 3' -GGCCAAAGG<sub>TT</sub> TGCTGTGA---F1'5' (179-49-01) b  
 3' -GGCCTAGG<sub>TT</sub> TGCTGTGA---F1'5' (192-72-04) c  
 3' -GGCCAAAGG<sub>TT</sub> TGCAGTGA F1'5' (192-72-05) d  
 3' -GGCCAAAGG-F15' (205-27-01) e

FIGURE 27

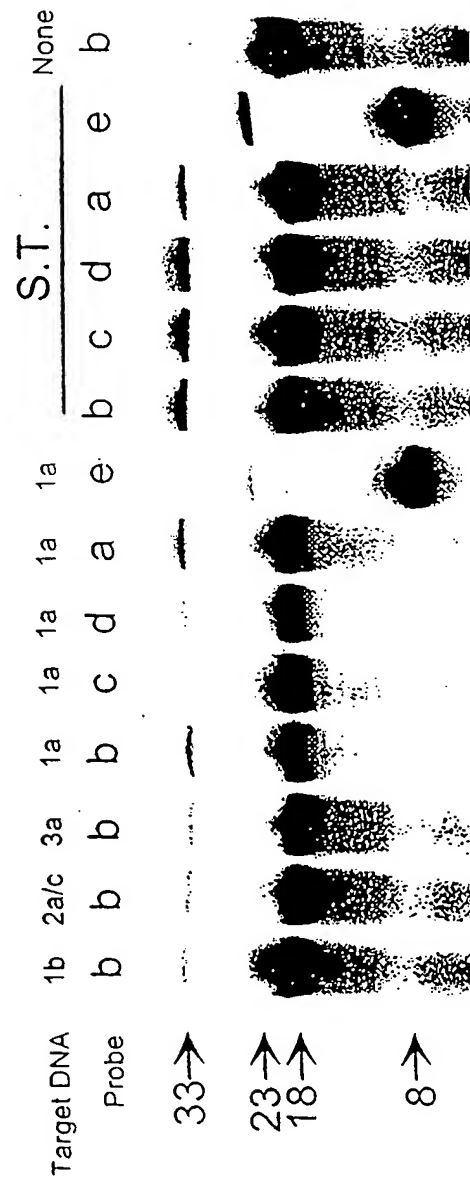


FIGURE 28

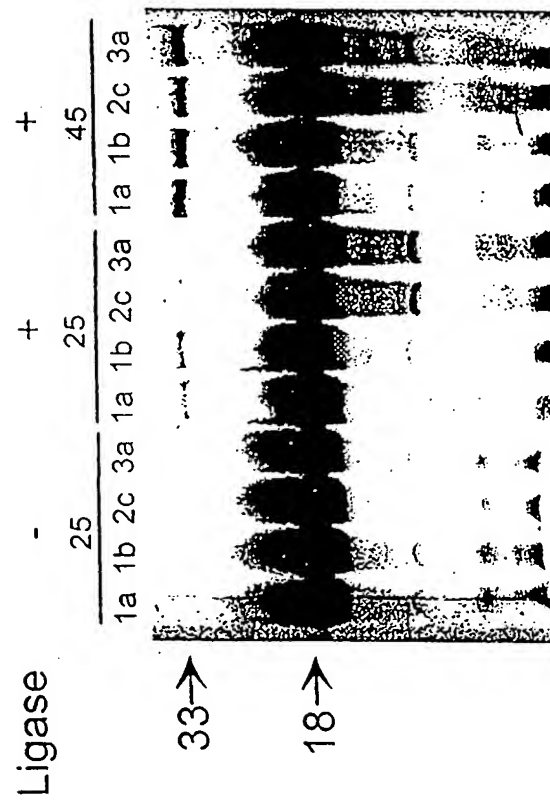
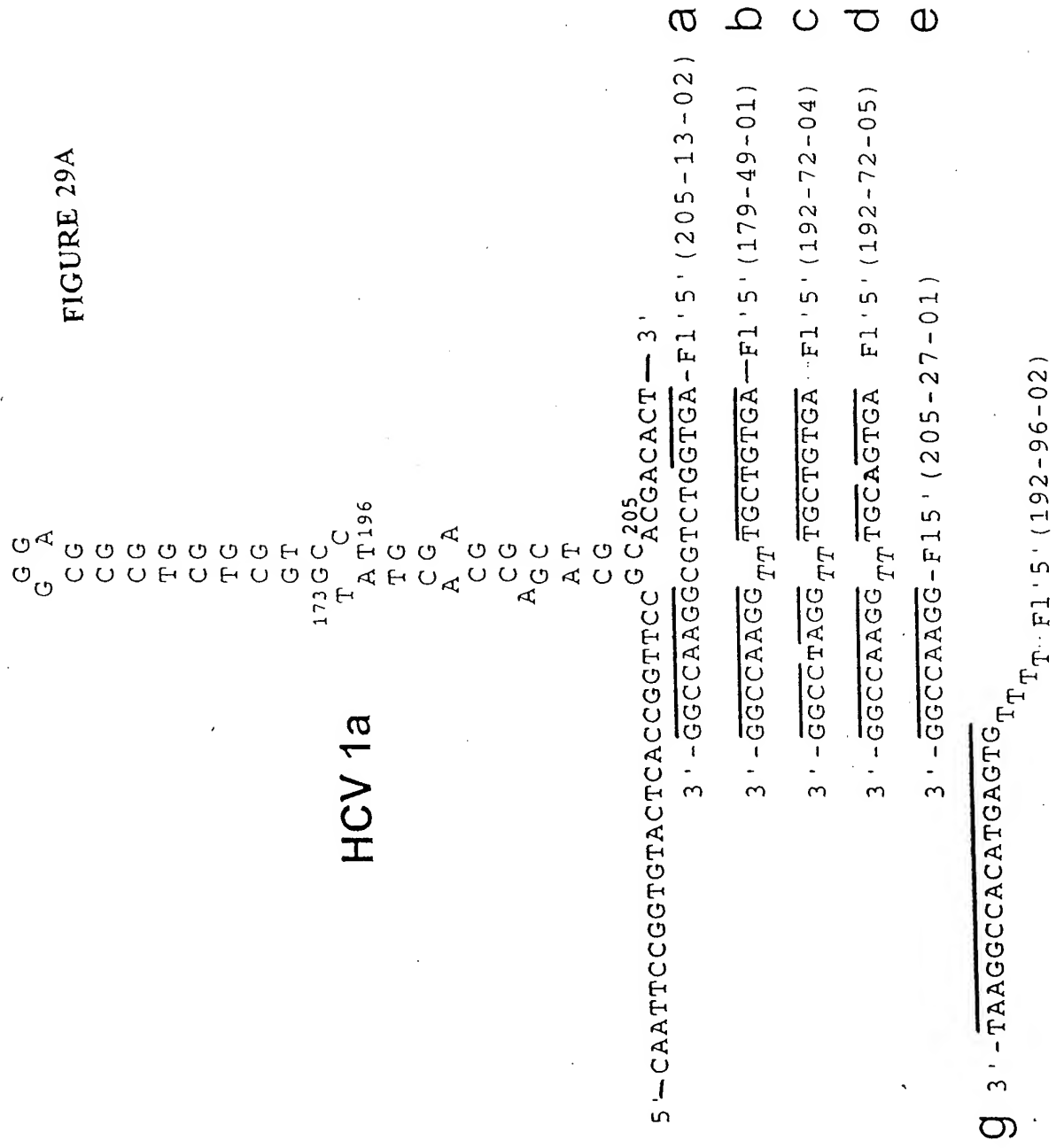


FIGURE 29A



5'-ATTCCGGTGTA<sup>C</sup>CTCA<sup>C</sup>CGGTTCCAAACGACACT-3' (205-13-01) S.T.

5'-ATTCCGGTGTA<sup>C</sup>CTCA<sup>C</sup>CGGTTCCAAACGACACT-3' (205-13-01) S.T.

3'-GGCCAAGGCGTCTGTGA-F1'5' (205-13-02) a

3' - GGCCAAGG TGCTGTGA TT - 5' (179-49-01) b

3' - GGCCTAGG T<sub>T</sub>TGCTGTGA - 5' (192-72-04) C

3'-GGCCAAGG<sub>TT</sub>TGCAGTGA--F1'5' (192-72-05) d

3' - GGCCAAGG - F15' (205-27-01)

g<sub>3</sub> - TAAGGCCACATGAGTG<sub>T</sub><sub>T</sub><sub>T</sub><sub>T</sub>...Fl'5' (192-96-02)

ITTT--F1'5' (192-96-02)

FIGURE 30

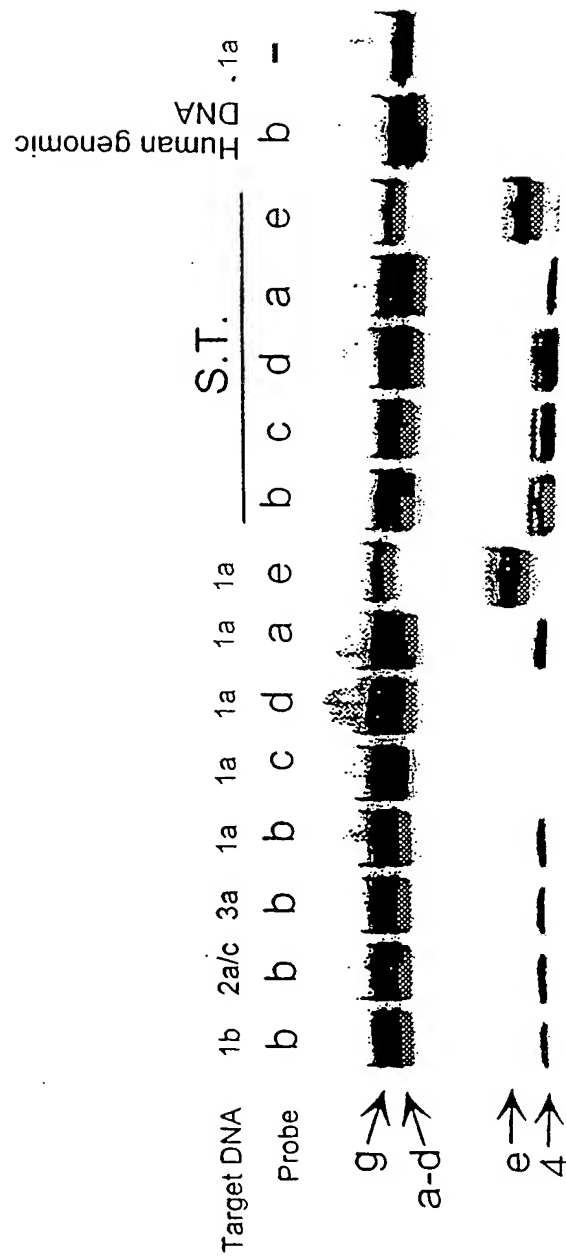


FIGURE 31

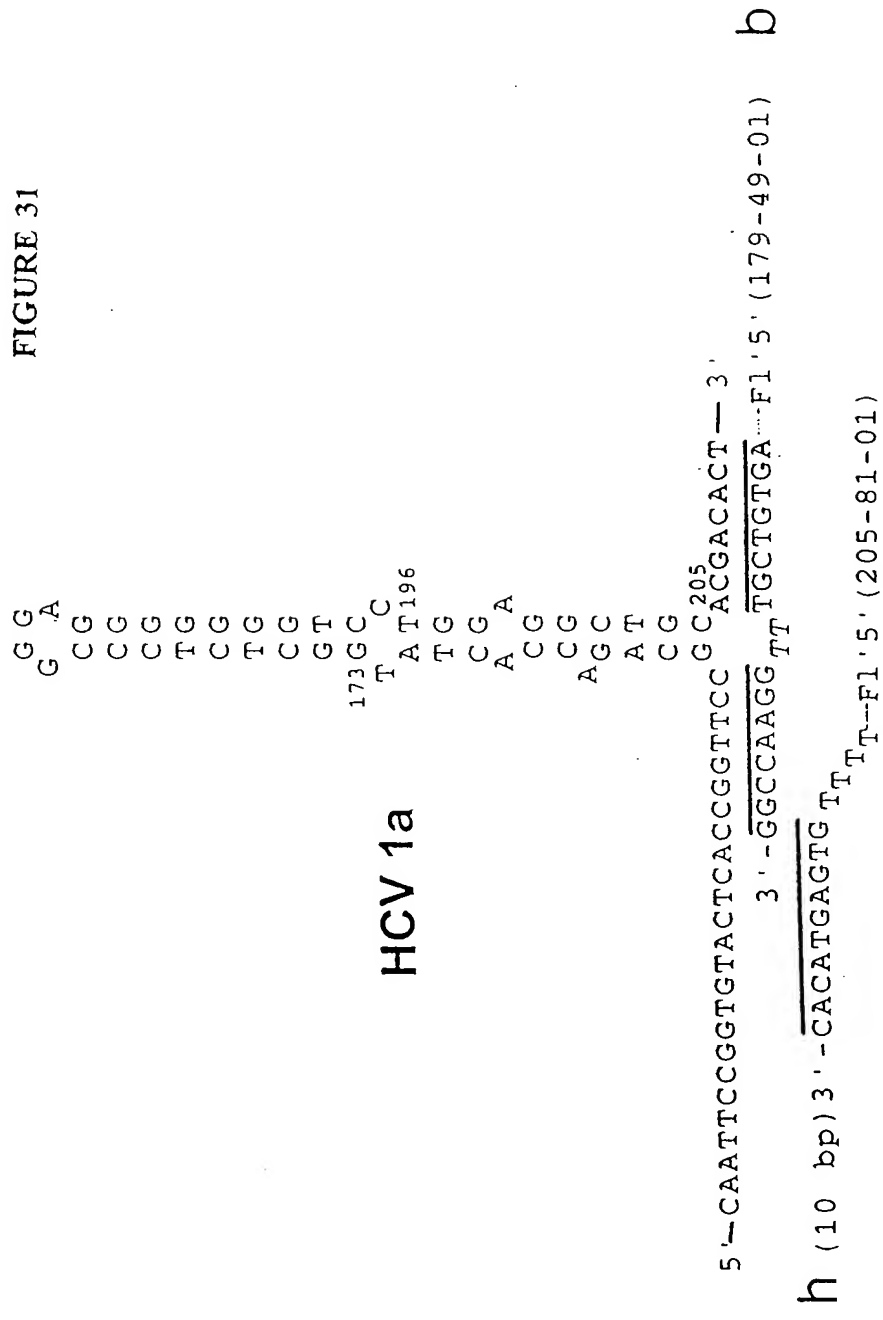


FIGURE 32

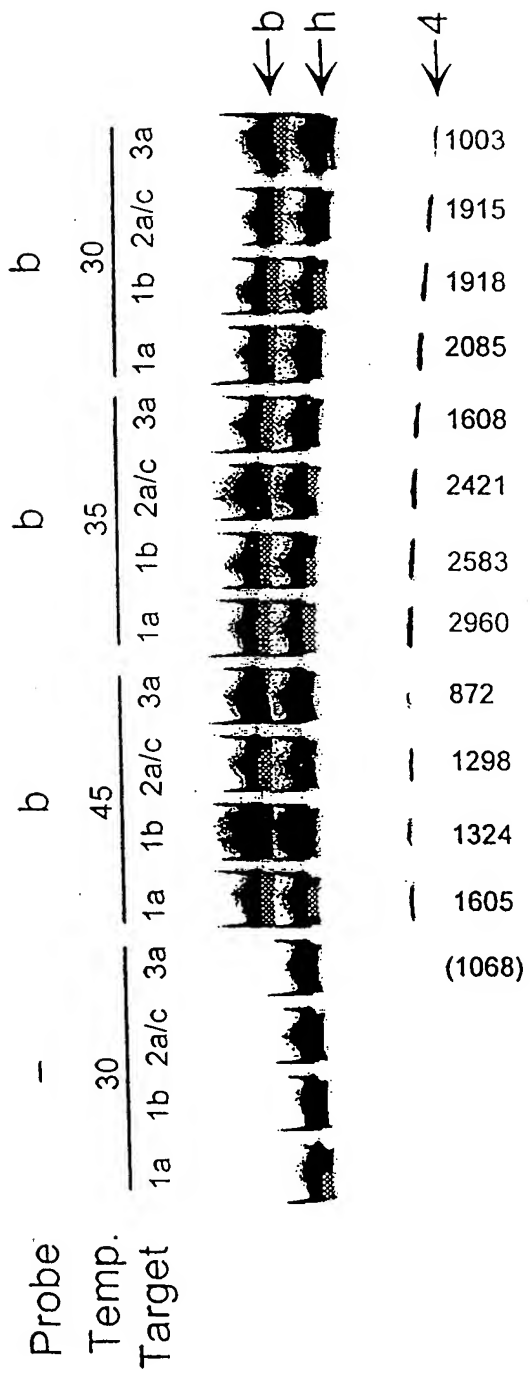




FIGURE 33

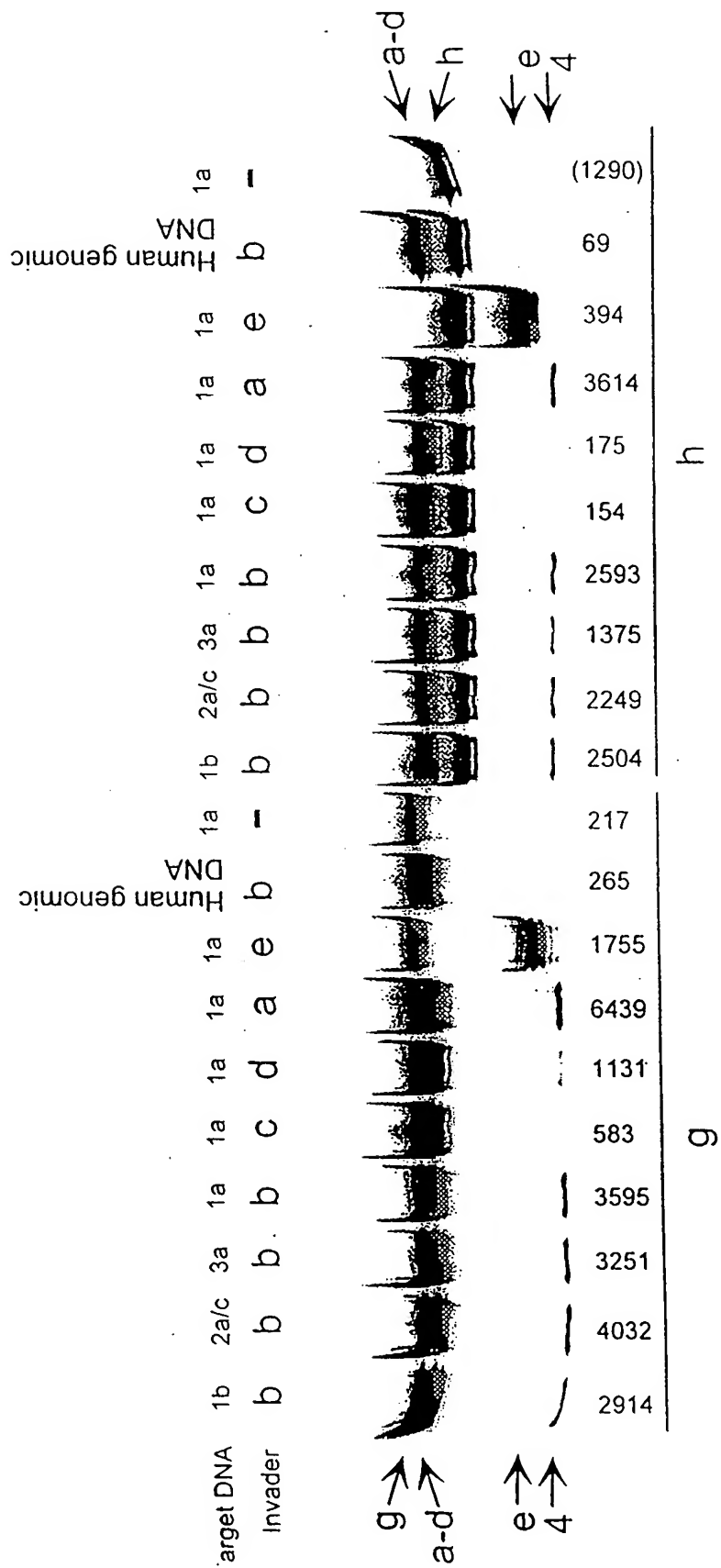
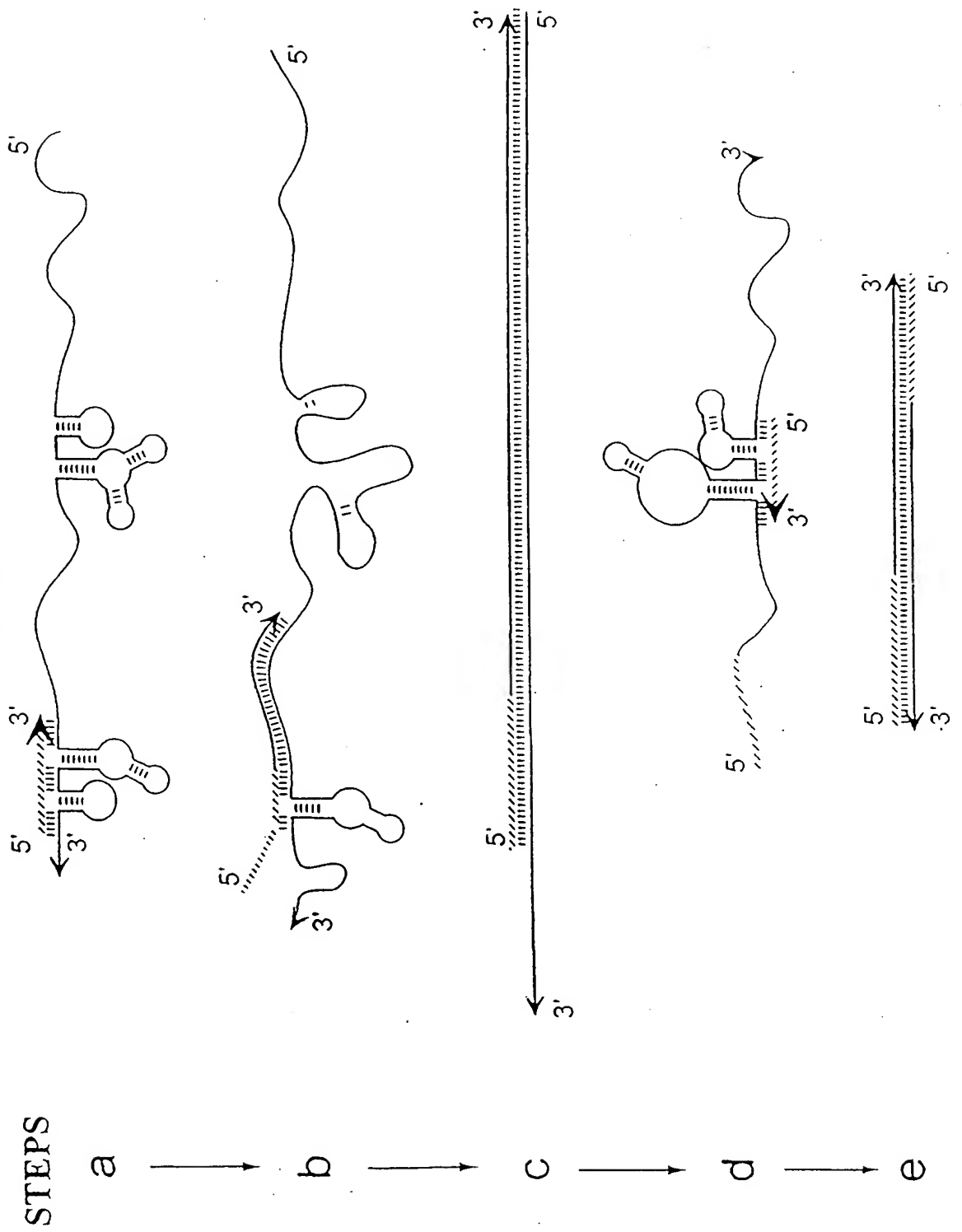


FIGURE 34



STEPS

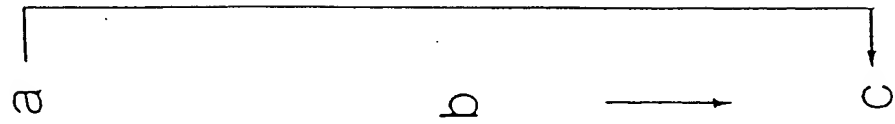


FIGURE 35

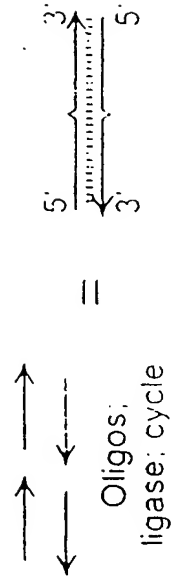
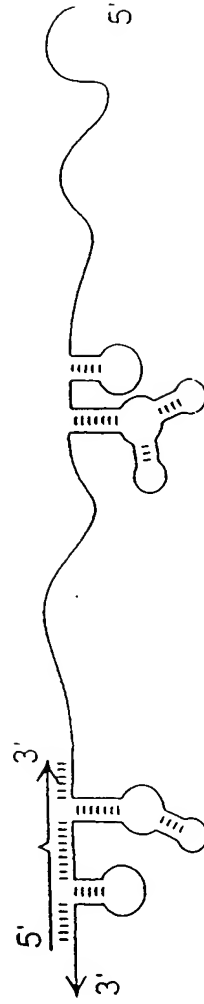
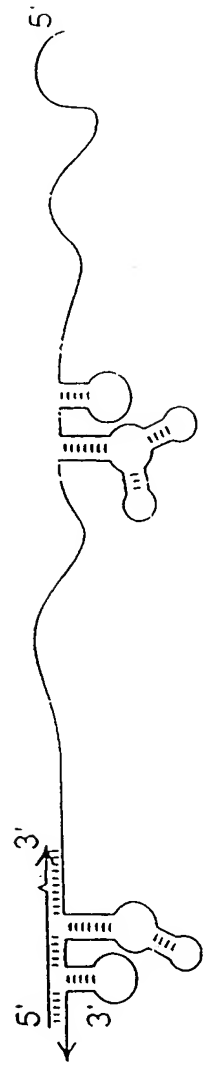


FIGURE 36

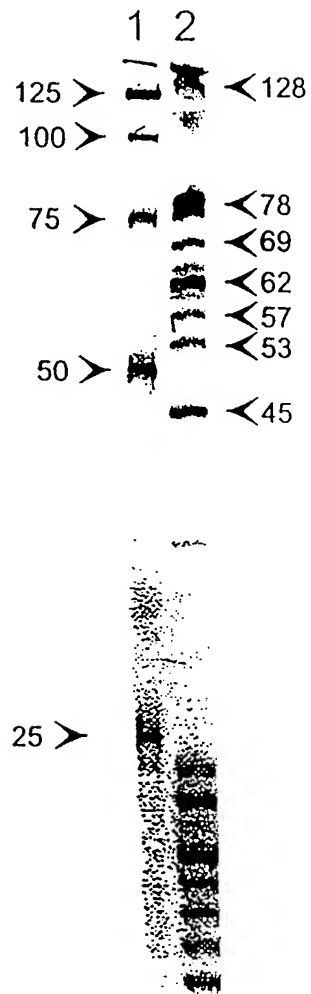


FIGURE 37A

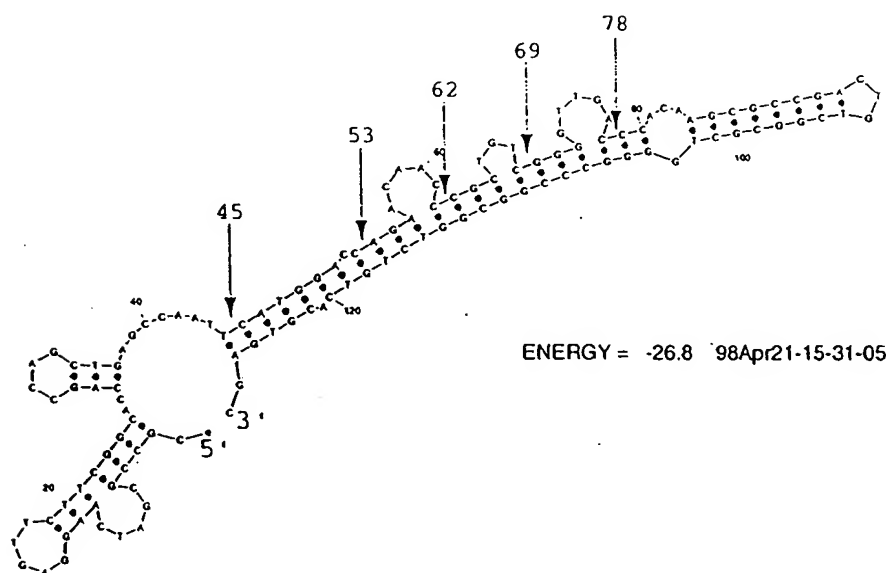
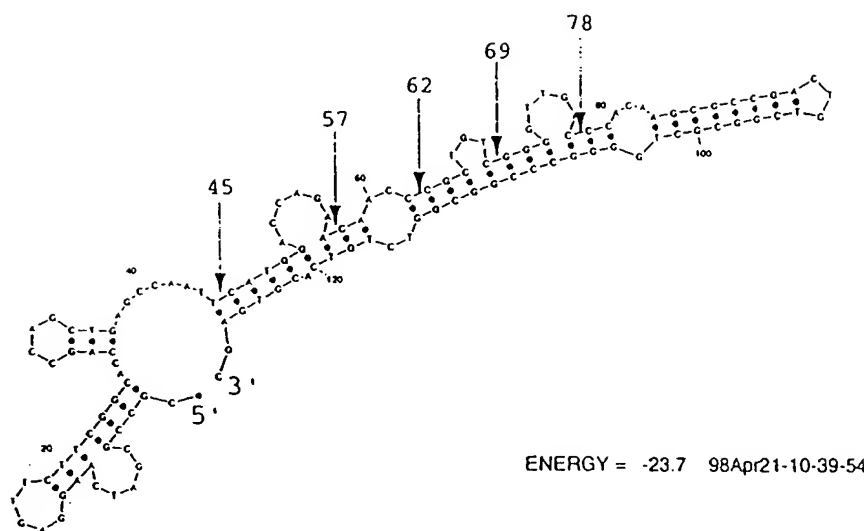


FIGURE 37B

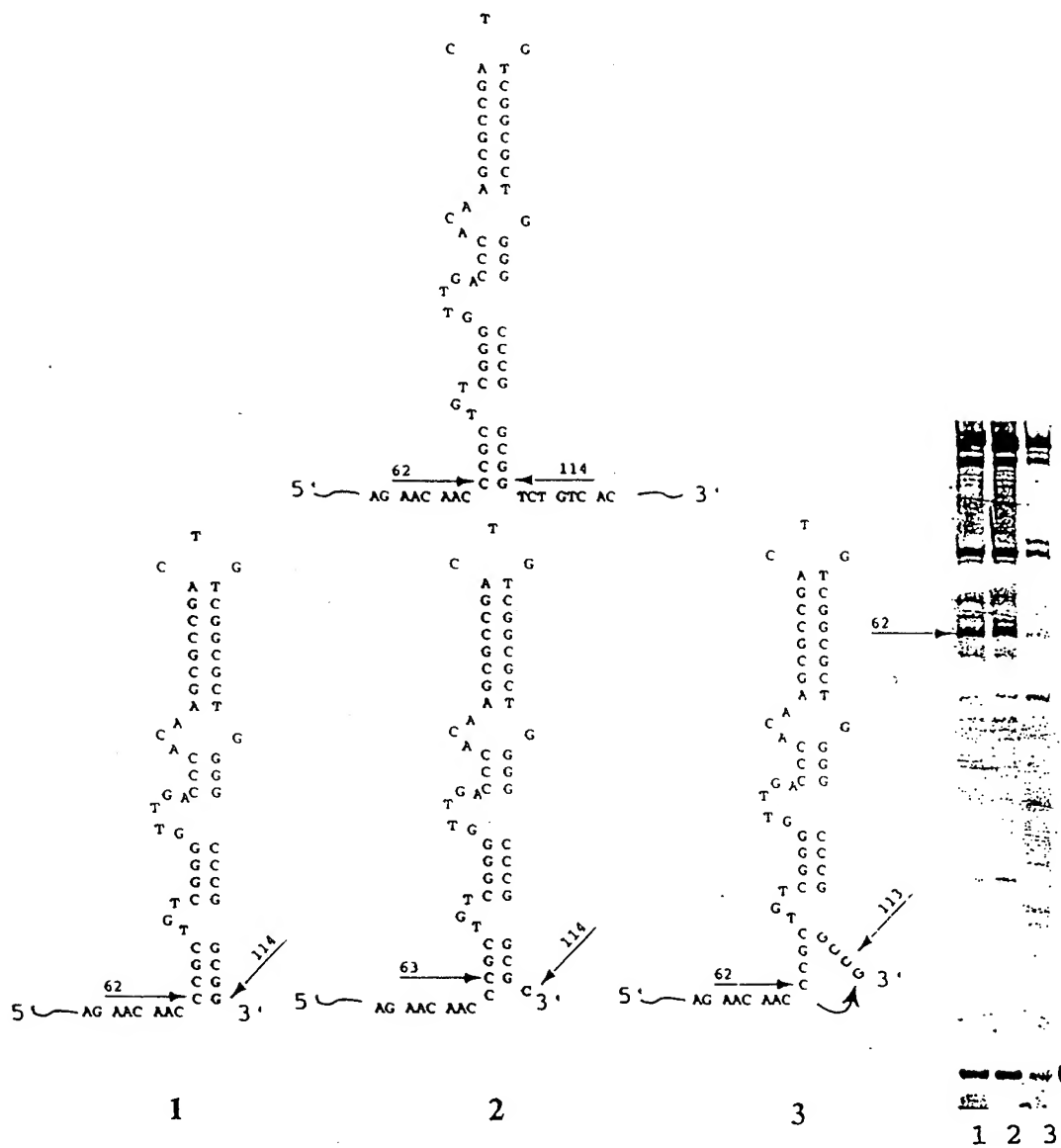
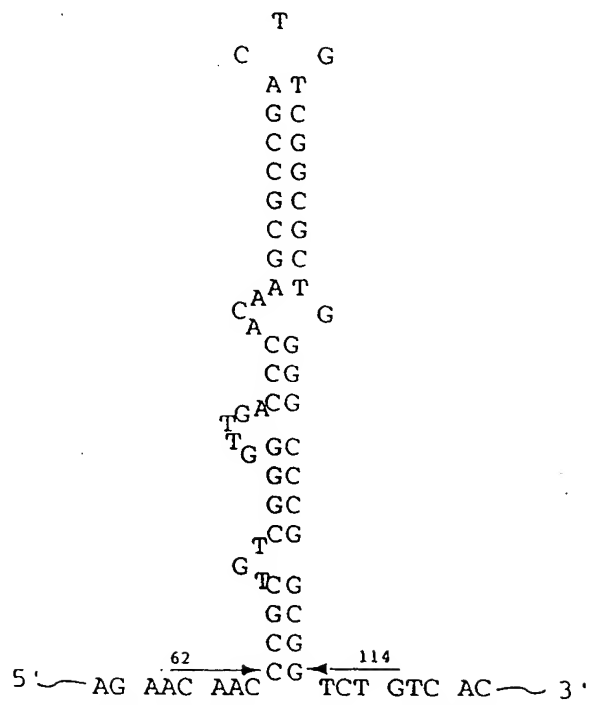


FIGURE 37C



62-114 a	3' TCT TGT TG	TT	AG ACA GTG 5'
62-114 b	TCT TGT TG		AG ACA GTG
62-114 c	TCT TGT TG	CG	AG ACA GTG
62-114 d	TCT TGT TG	AA	AG ACA GTG
62-114 e	TCT TGT TG	DD	AG ACA GTG

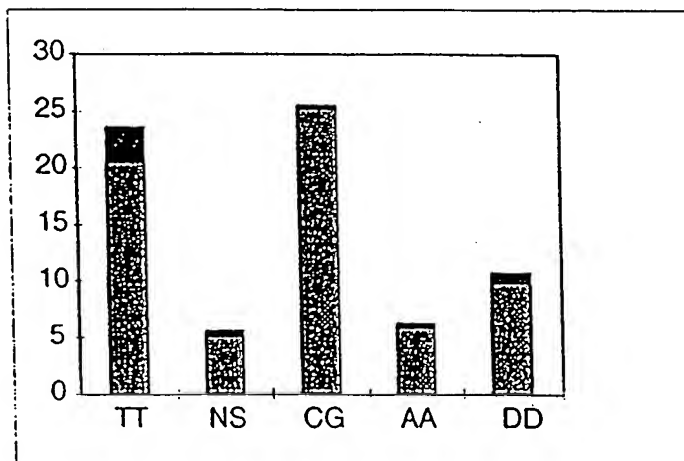


FIGURE 38A

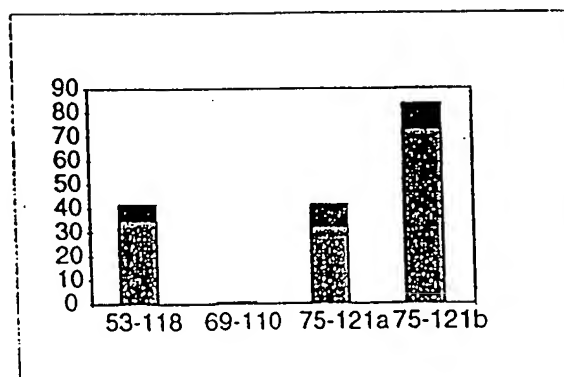
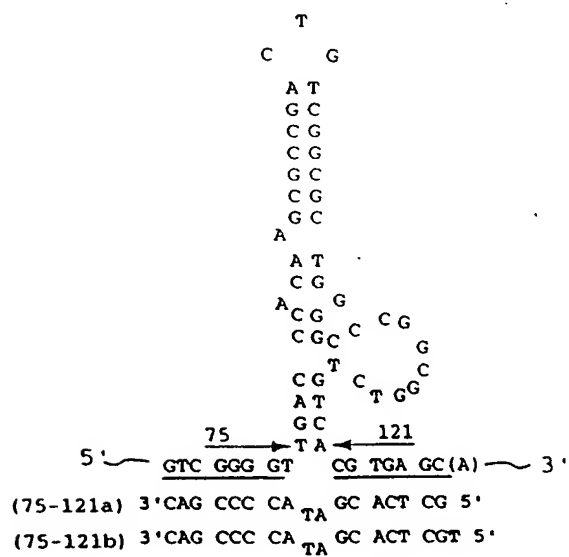
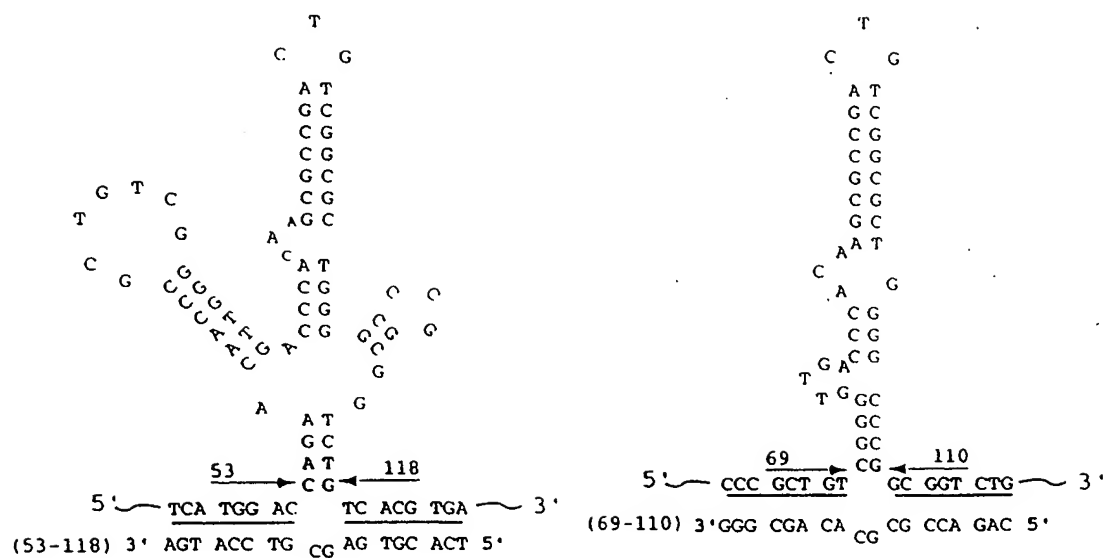
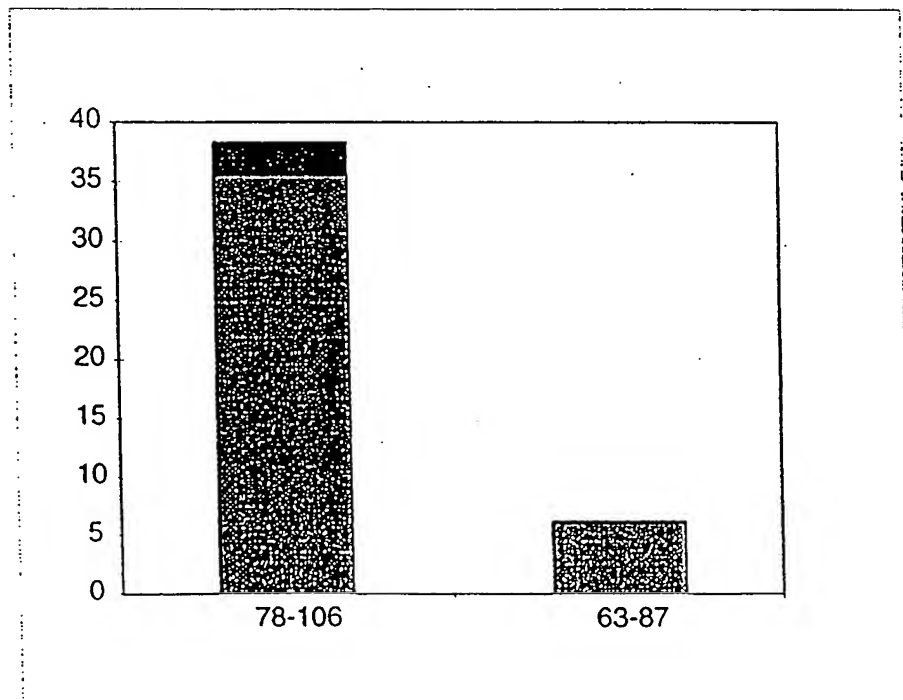
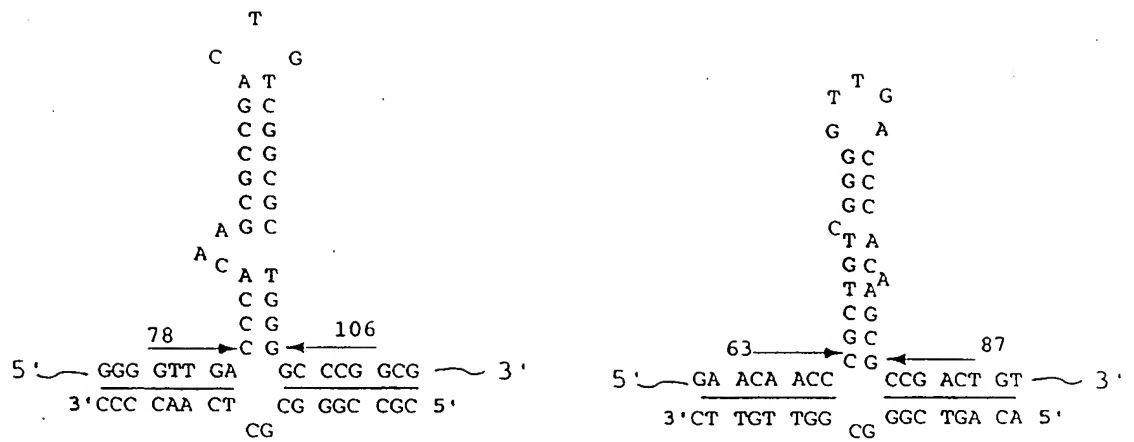
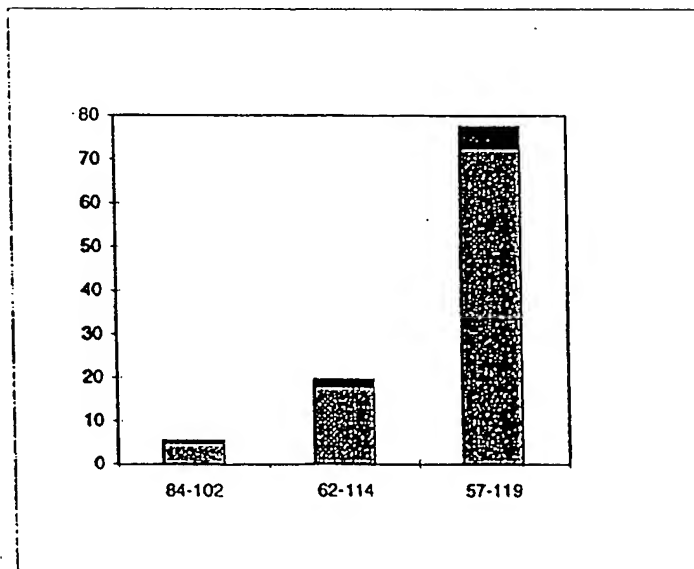
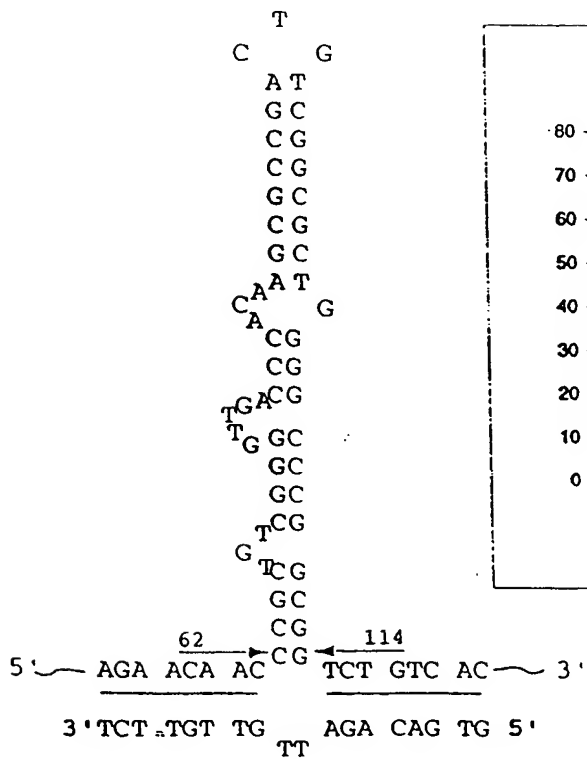
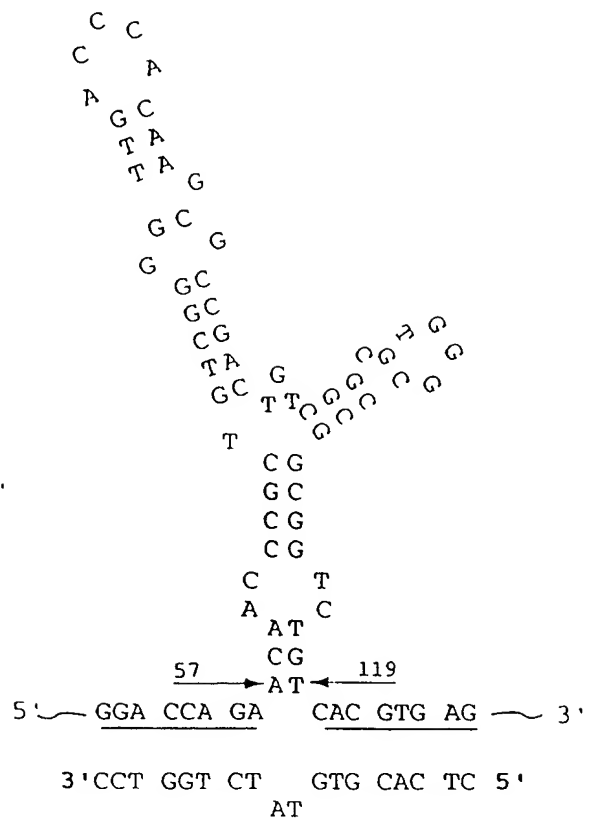
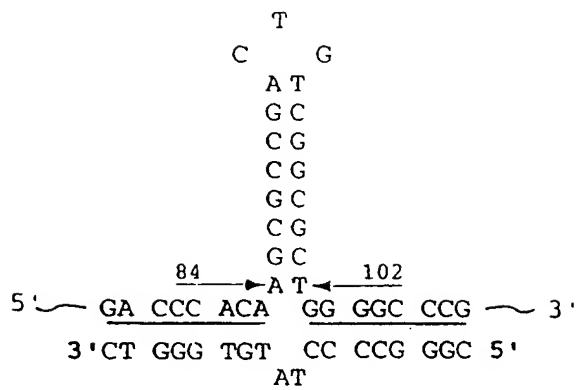




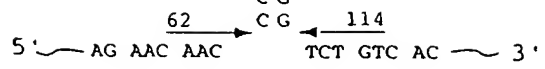
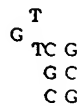
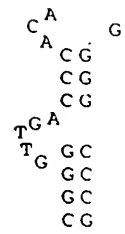
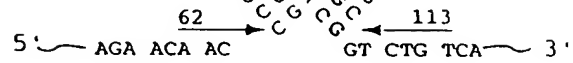
FIGURE 38B



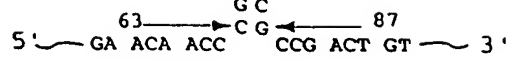
**FIGURE 38C**



T	
C	G
A	T
G	C
C	G
C	G
G	C
C	G
G	C
A	T

[illegible]

T<sup>T</sup> G  
 G A  
 GC  
 GC  
 GC  
 CTA  
 GC<sup>A</sup>  
 TA<sup>A</sup>  
 CG  
 GC  
 CG



(c)

FIGURE 40

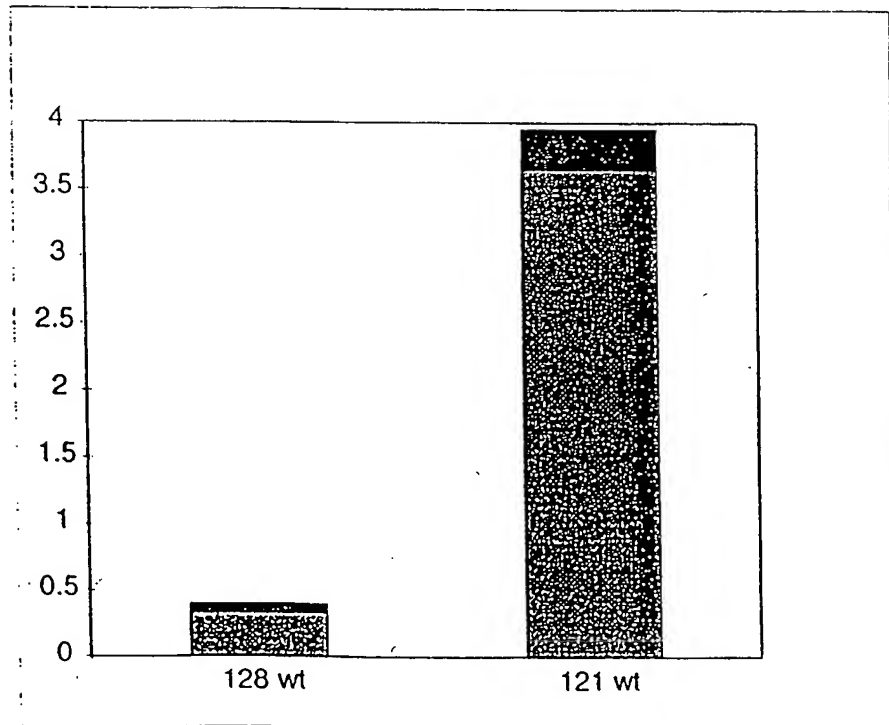
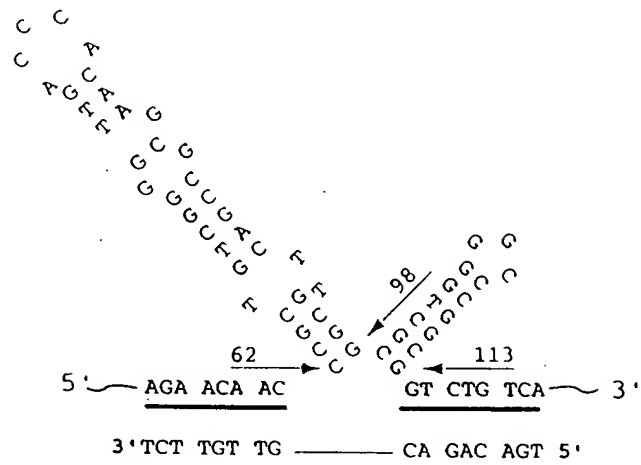


FIGURE 41

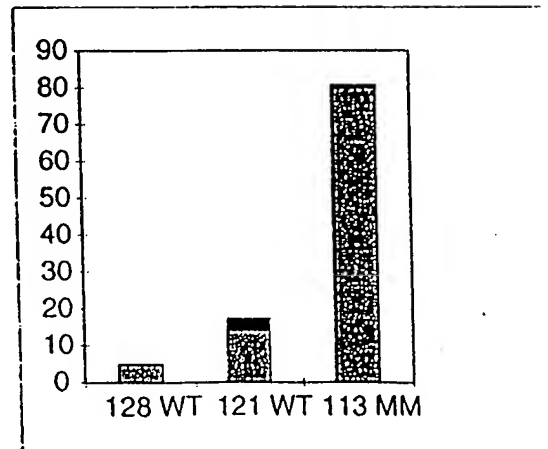
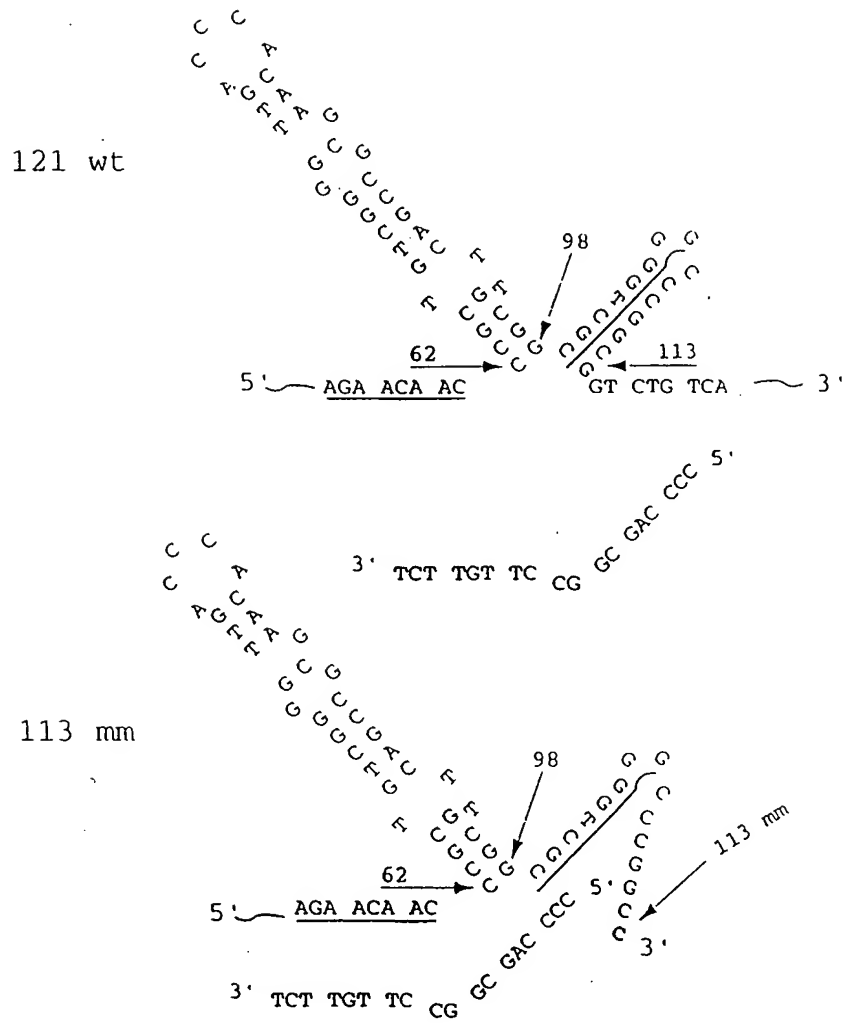


FIGURE 42

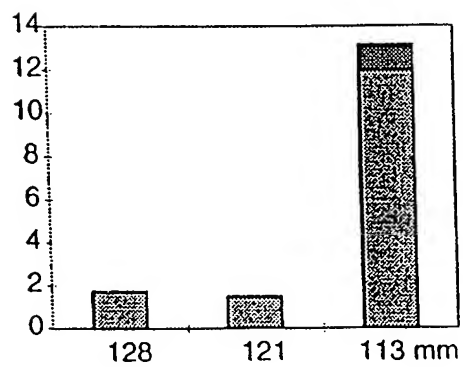
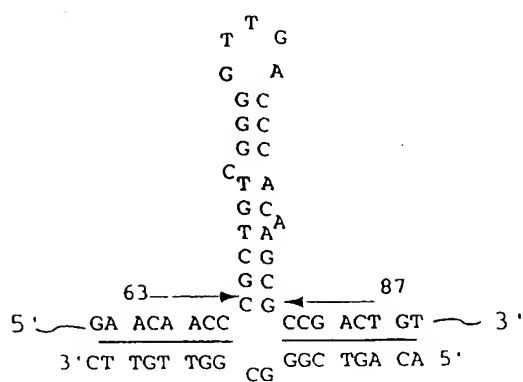


FIGURE 43A

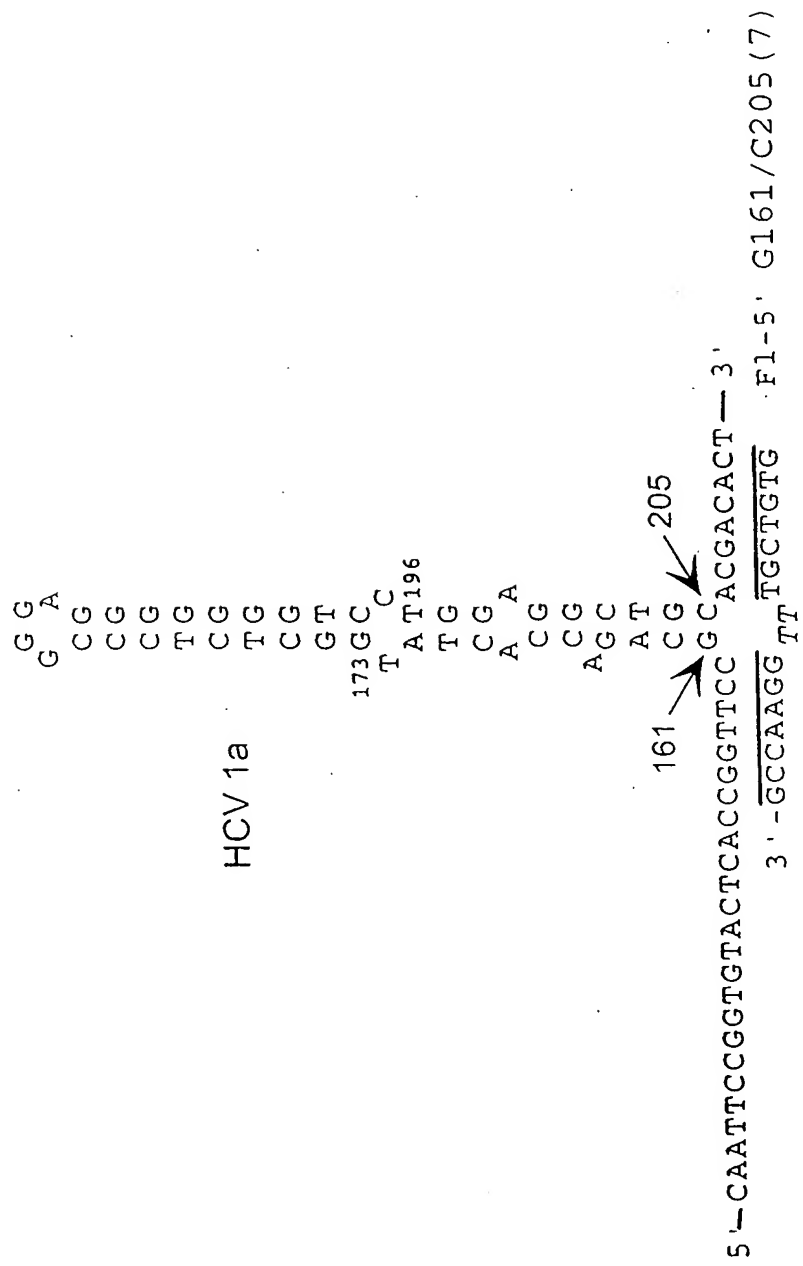


FIGURE 43B

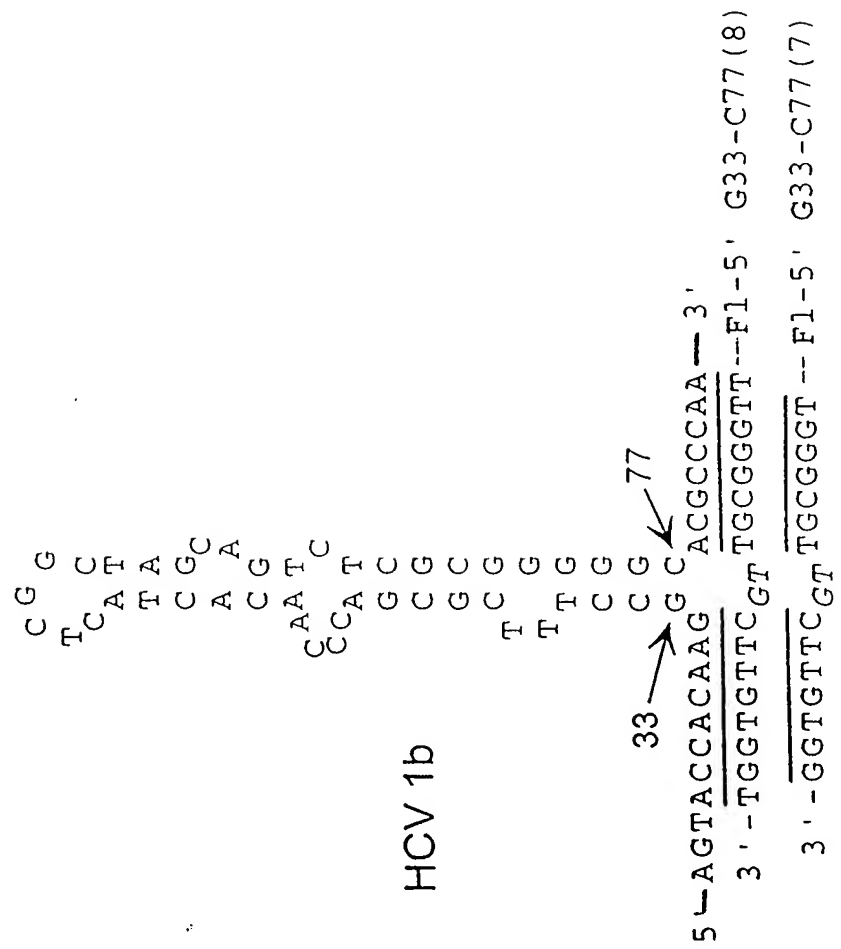




FIGURE 44A

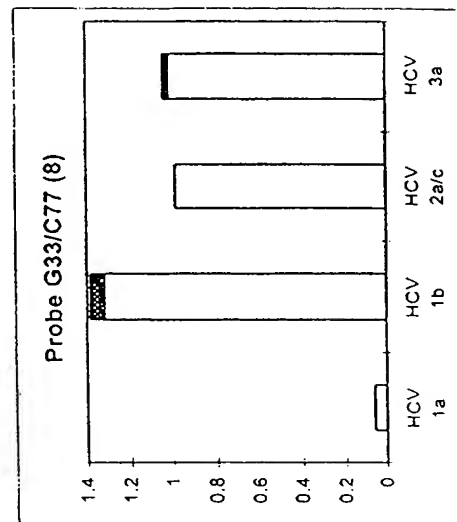
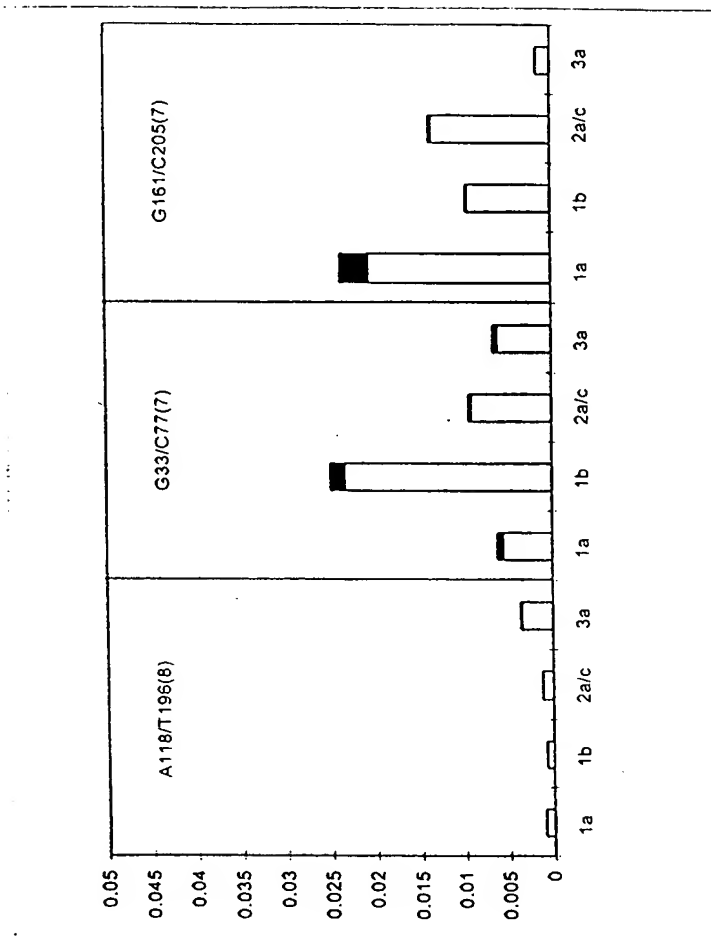


FIGURE 44B



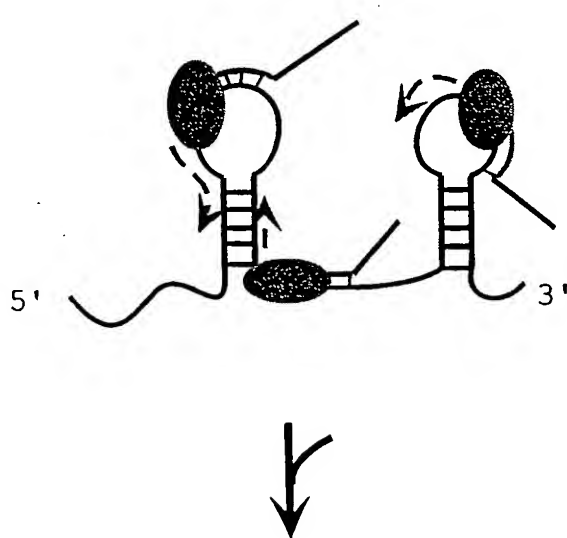
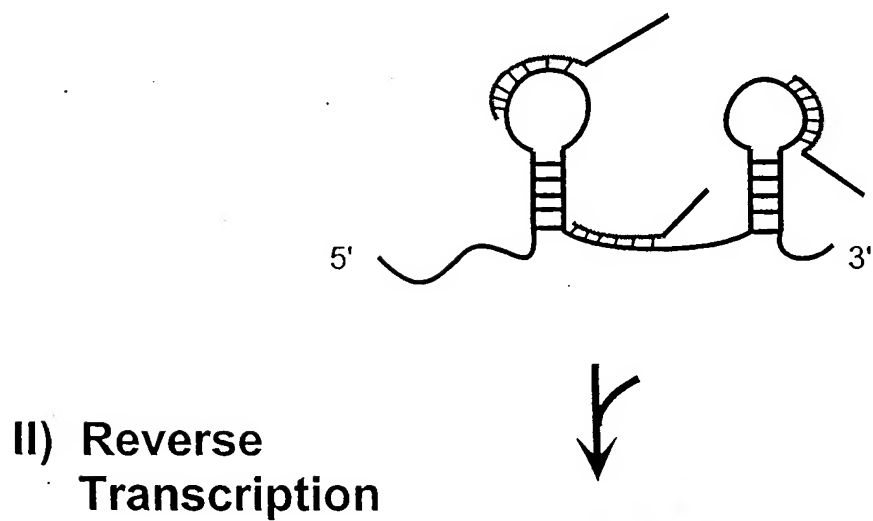
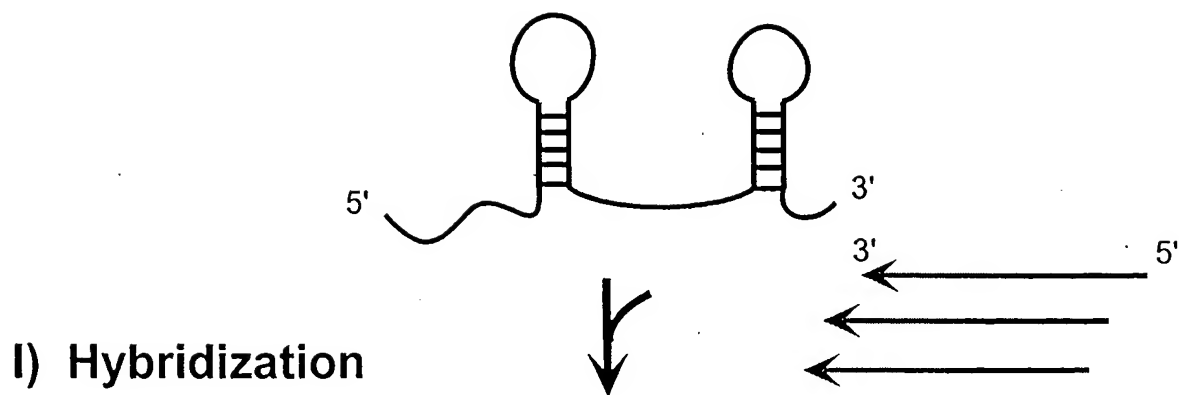
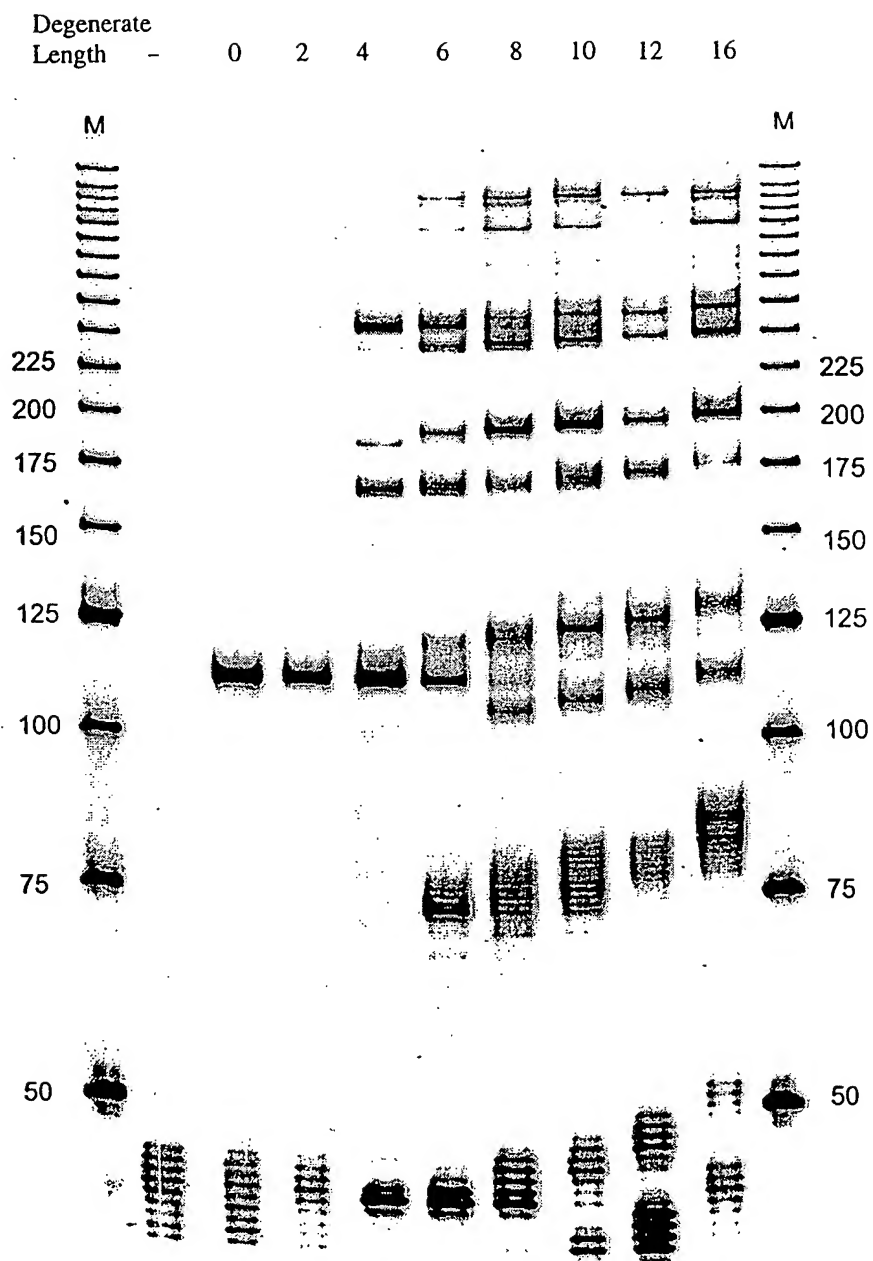


FIGURE 45A



**FIGURE 46**



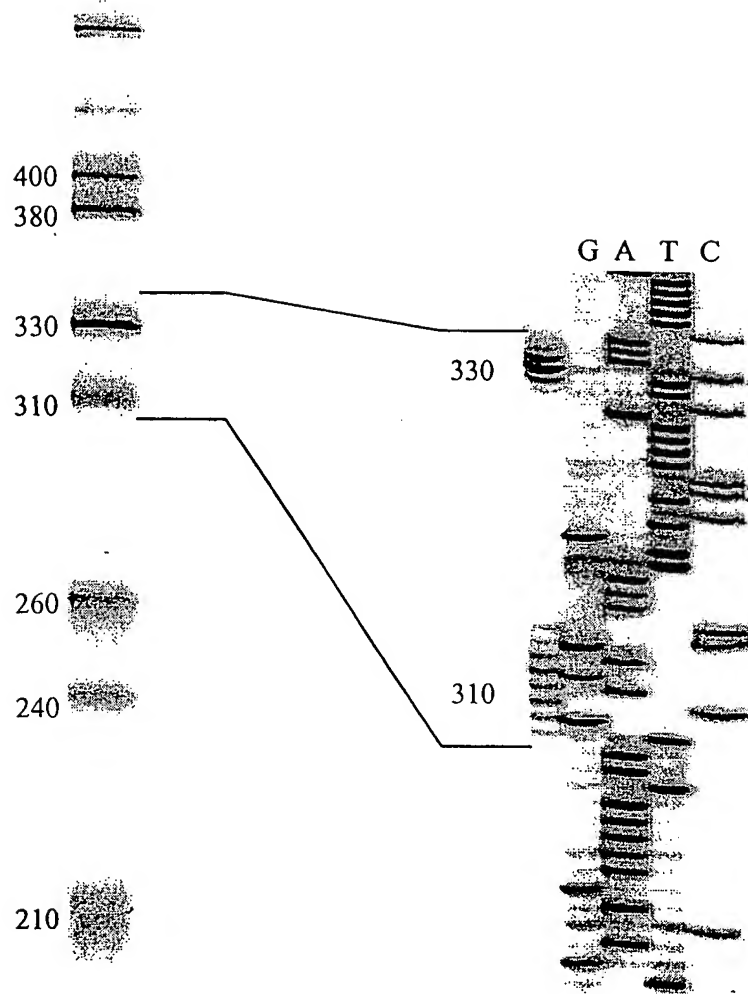


FIGURE 47

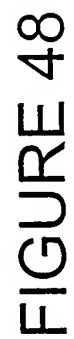


FIGURE 48

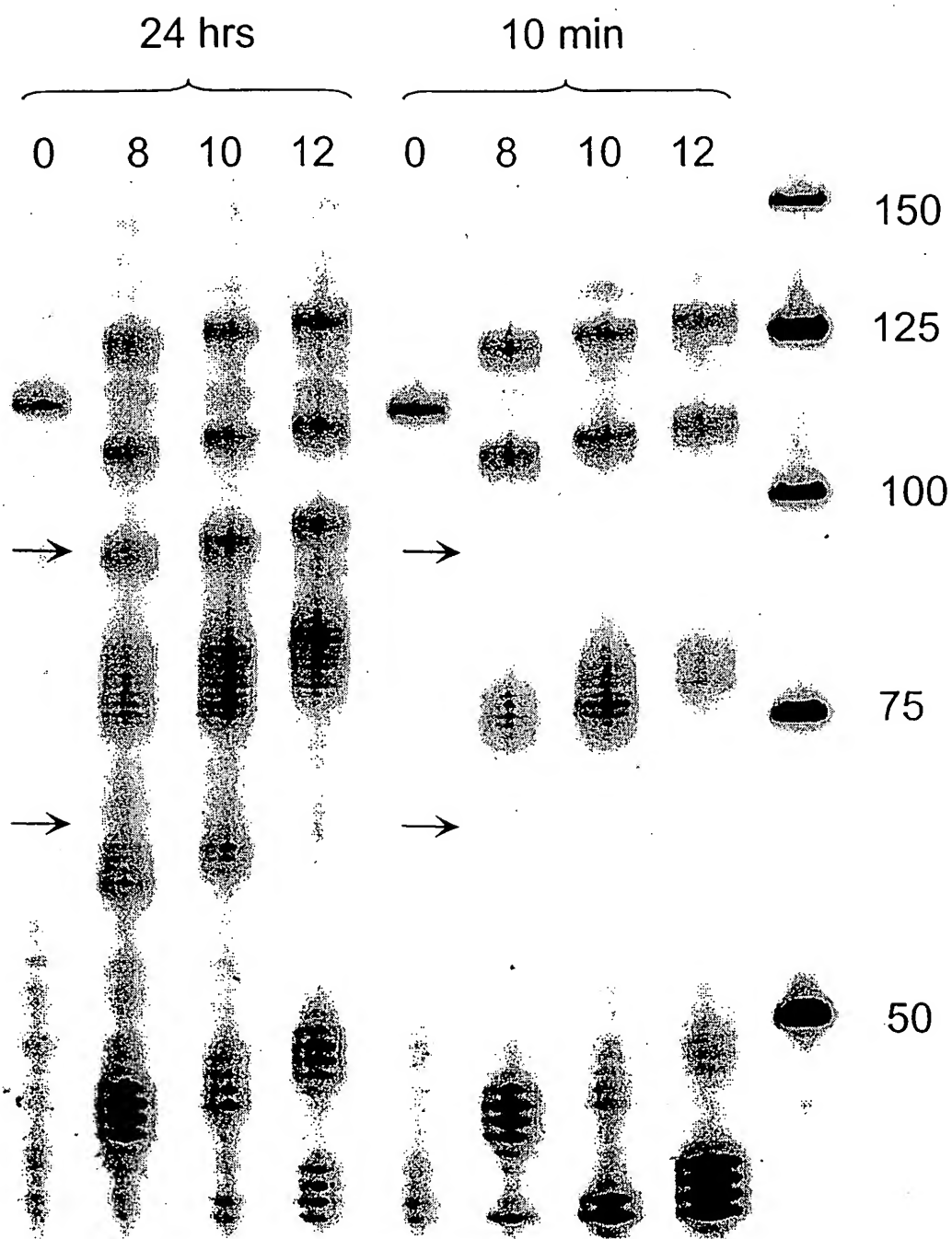


FIGURE 49



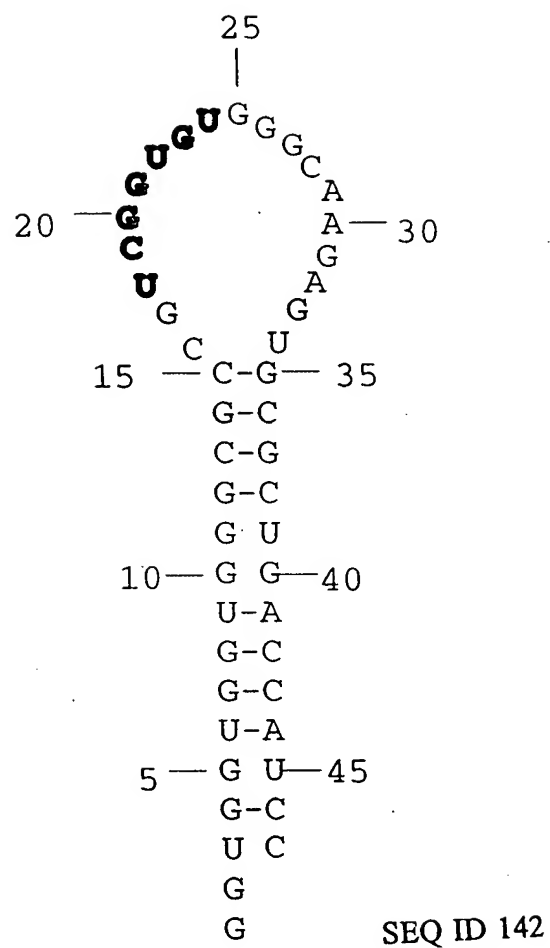


FIGURE 50A

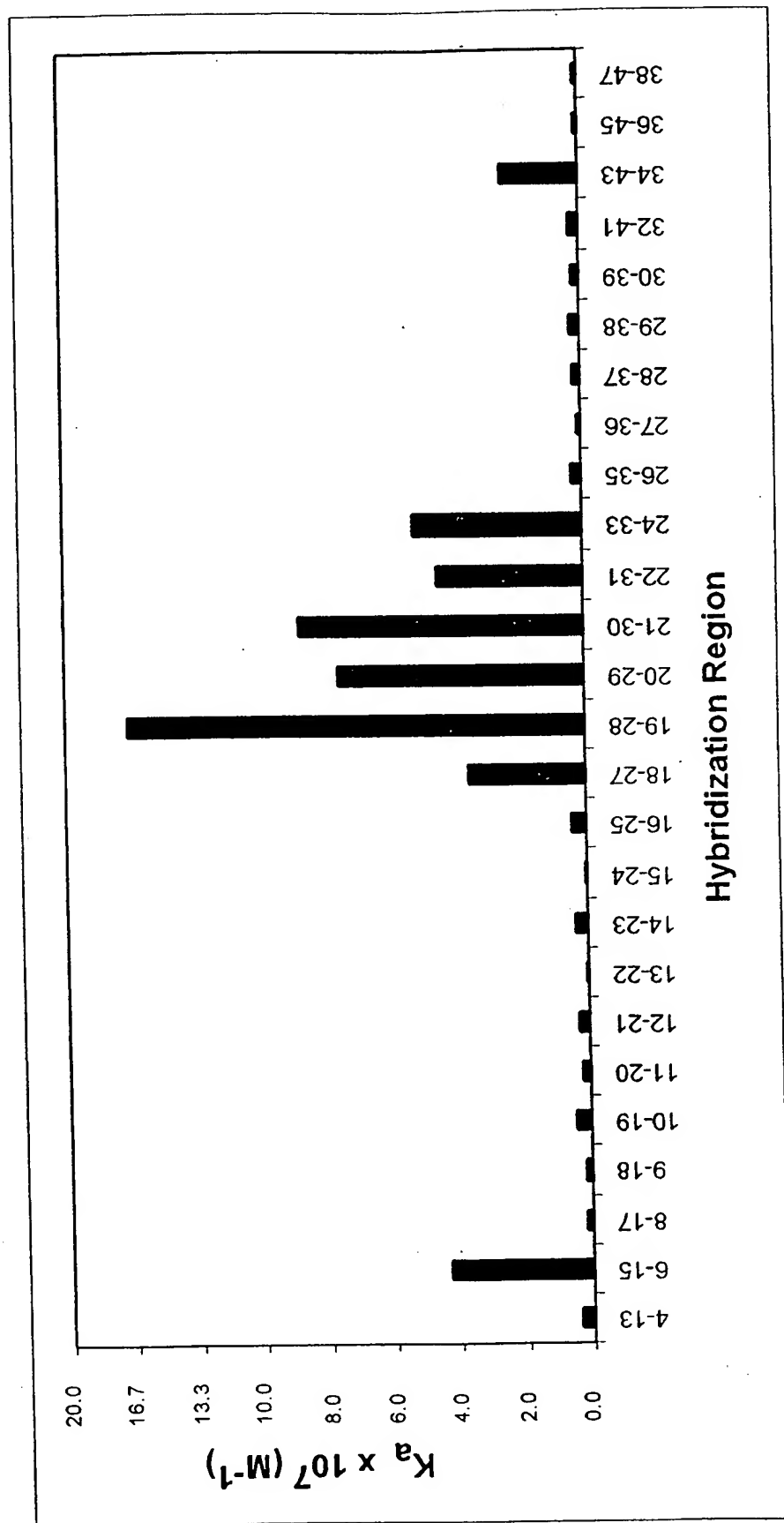


FIGURE 50B

## FIGURE 51

1 ACACUUGCUU UUGACACAAC UGUGUUUACU UGCA**AAUCCCC** CAAAACAGAC

64-68 88-97

51 AGA**AUGGUGC** AUCUGUCCAG UGAGGAGA**AAG UCUGCGGUCA** CUGCCCUGUG

101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC

151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGUCCUU UGGGGACCUG

## FIGURE 52A

ISIS 1571(-) ISIS 3067(+)  
1 GCGCCCC AGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT

ISIS 1570(+)  
41 GCA**ACCTCAG** CCTCGCTATG GCTCCCAGCA GCCCCCGGCC  
81 CGCGCT**GCCC** GCACTCCTGG TCCTGCTCGG GGCTCTGTTC  
121 CCAGGACCTG GCAATGCCCA GACATCTGTG **TCCCCCTCAA**  
161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACATG  
201 **CAGCACCTCC** TGTGACCAGC **CCAAGTTGTT** GGGCATAGAG  
241 **ACCCCGTTGC** CTAAAAAGGA GTTGCTCCTG CCTGGGAACA  
281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934(-)  
321 CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA  
361 ACAGCTAAAA **CCTTCCTCAC** CG**TGTACTGG** ACTCCAGAAC  
401 GGGTGGA**ACT** **GGCACCCCTC** CCCTCTTGGC AGCCAGTGGG  
441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGG**CA**  
481 **CCCCGGGCCA** ACCTCACCGT GGTGCTGCTC CGTGGGGAGA

## FIGURE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA  
as 610  
561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA  
601 GCCAATTTCT **CGTGCCGCAC** TGA ACTGGAC CTGCGGCCCC  
641 AAGGG**CTGGA** GCTGTTTGAG AAC**ACCTCGG** CCCCCTACCA  
681 GCTCCAGACC TTTGTCCT**TGC** **CAGCGACTCC** CCCACA ACTT  
721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG  
761 TGGTCTGTTC CCT**TGGACGGG** CTGTTCCCAG TCT**CGGAGGC**  
801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC  
841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT  
881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT  
921 GACGTGTGCA GTAATACTGG GGA**ACCAGAG** **CCAGGAGACA**  
961 CTGCAGACAG **TGACCATCTA** CAGCTTTCCG **GCGCCCAACG**  
1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

## FIGURE 52C

1041 GACAGTGAAG TGT**GAGGCC** ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA **ACGGGCGCAG**

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 **ATACACAAGA** ACCAGACCCG GGAGCTTCGT GTCCTGTAT**G**

1241 **GCCCCCGACT** GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGGCCAGAA AATT**CCCAGC** **AGACTCCAAT** GTGCCAGGCT

1321 TGGGGGAACC CATTGCCCGA GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTT**TCCC** ACTGCCCATC **GGGGAATCAG** TGACTGTCAC

1401 TCGAGATCTT **GAGGGCACCT** ACCTCTGTCG GGCCAGGAGC

1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC **ATAATGGGCA** CT**GCAGGCCT** **CAGCACGTAC**

## FIGURE 52D

1561 CTCT**ATAACC** **GCCAGCGGAA** GATCAAGAAA TACAGACTAC

as 1630 as 1630h(+++)

1601 **AACAGGCCCA** **AAAAGGGACC** **CCCATG****AAAC** **CGAACACACA**

ISIS 1938 (+)

1641 **AGCCAC****GCCT** **CCCTGAACCT** **ATCCCGGGAC** **AGG**GCCTCTT

1681 **CCTCGGCCTT** CCCATATTGG TGGCAGTGGT **GCCACACTGA**

1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCT**ACCGG**

1761 **CCCTGGGACG** CCGGAGGACA GGGCATTGTC CTCAGTCAGA

1801 **TACAACAGCA** **TTTGGGGCCA** TGGTACCTGC **ACACCTAAAA**

1841 CACT**AGGCCA** **CGCATCTGAT** CTGTAGTCAC ATGACTAAGC

1881 CAAGAGGA**AG** **GAGCAAGACT** CAAGACATGA TTGATGGATG

ISIS 1939 (+)

1921 TTAAAGTCTA GCCTGAT**GAG** **AGGGGAAGTG** GTGGGGGAGA

1961 CATAGCCCCA CCAT**GAGGAC** ATAC**AACTGG** GAAATACTGA

2001 AACTTGCTGC CTATTGGGTA TGCT**GAGGCC** CACAGACTTA

2041 CAGAAG**AGT** **GGCCCTCCAT** AGACATGTGT AGCATCAAAA

## FIGURE 52E

ISIS 2302 (+)

2081 CACAAAGGCC CACACTTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGTCTA CTGACCCCAA CCCTTGATGA TATGTATTTA

ISIS 1572

2161 TTCATTTGTT ATTTTACCAG CTATTTATTG AGTGTCTTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT AACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CAAATGGGGC TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTTC TATCGGCACA AAAGCACTAT

2401 ATGGACTGGT AATGGTTCAC AGGTTCAGAG ATTACCCAGT

2441 GAGGCCTTAT TCCTCCCTTC CCCCCAAAAC TGACACCTTT

2481 GTTAGCCACC TCCCCACCCA CATACATTTT TGCCAGTGTT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC

2561 AGGGAATATG CCCAAGCTAT GCCTTGTCCT CTTGTCCTGT



## FIGURE 52F

2601 TTGCATTTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

# FIGURE 53A

1 CACAUUGUUC UGAUCAUCUG AAGAU CAGCU AUUAGAAGAG  
 41 AAAGAU CAGU UAAGUCCUUU GGACCUGAUC AGCUUGAUAC site 80  
 81 AAGAACUACU GAUUUCAACU UCUUUGGCUU AAUUCUCUCG site 120  
 121 GAAACGAUGA AAUAUACAAG UUAUAUCUUG GCUUUUCAGC  
 161 UCUGCAUCGU UUUGGGUUCU CUUGGCUGUU ACUGCCAGGA  
 201 CCCAU AUGUA CAAGAAGCAG AAAACCUUAA GAAAU AUUUU site 210  
 241 AAUGCAGGUC AUUCAGAUGU AGCGGAUAAU GGAACUCUUU site 240 site 260  
 281 UCUUAGGCAU UUUGAAGAAU UGGAAAGAGG AGAGUGACAG  
 321 AAAAAUAAUG CAGAGCCAAA UUGUCUCCUU UUACUUCAAA site 330  
 361 CUUUUUAAAA ACUUUAAAGA UGACCAGAGC AUCCAAAAGA site 380 site 400  
 401 GUGUGGAGAC CAUCAAGGAA GACAUGAAUG UCAAGUUUUU  
 441 CAAUAGCAAC AAAAAGAAAC GAGAUGACUU CGAAAAGCUG

FIGURE 53B

481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG

521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC site 560

561 AGCAGCUAAA ACAGGGAAGC GAAAAAGGAG UCAGAUGCUG site 570

601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC

641 UACAAUUAUU GAAUUUUAUA UCUAAAUCUA UUUAUUAUA

681 UUUAACAUA UUUAUAUGGG GAAUAUAUUU UUAGACUCAU

721 CAAUCAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG

761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUAU UUAUAAUCC

801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA

841 CUAUUAGGC AAGGCUAUGU GAUUACAAGG CUUUAUCUCA site 850 site 860 site 880

881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG site 890 site 910

921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUAU

961 AAGUGAAGUG AUACUAUCCA GUUACUA

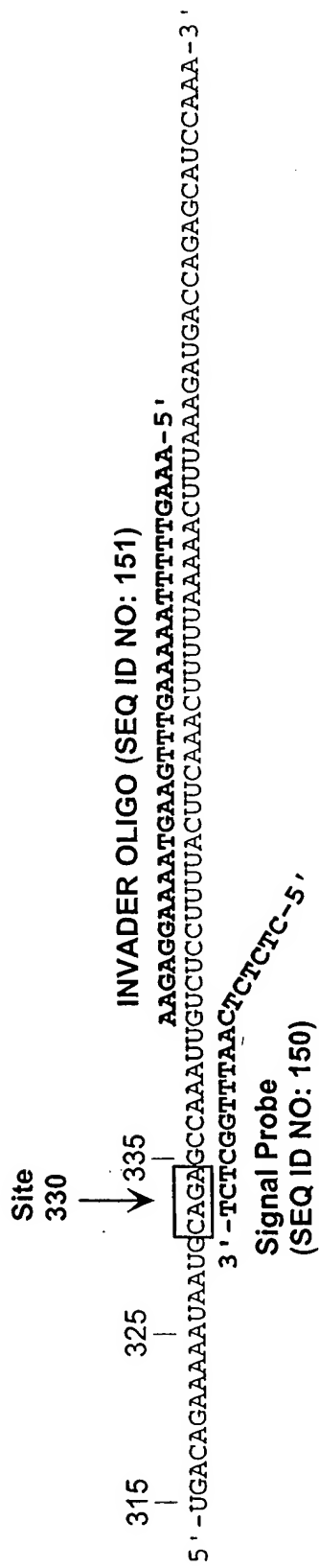
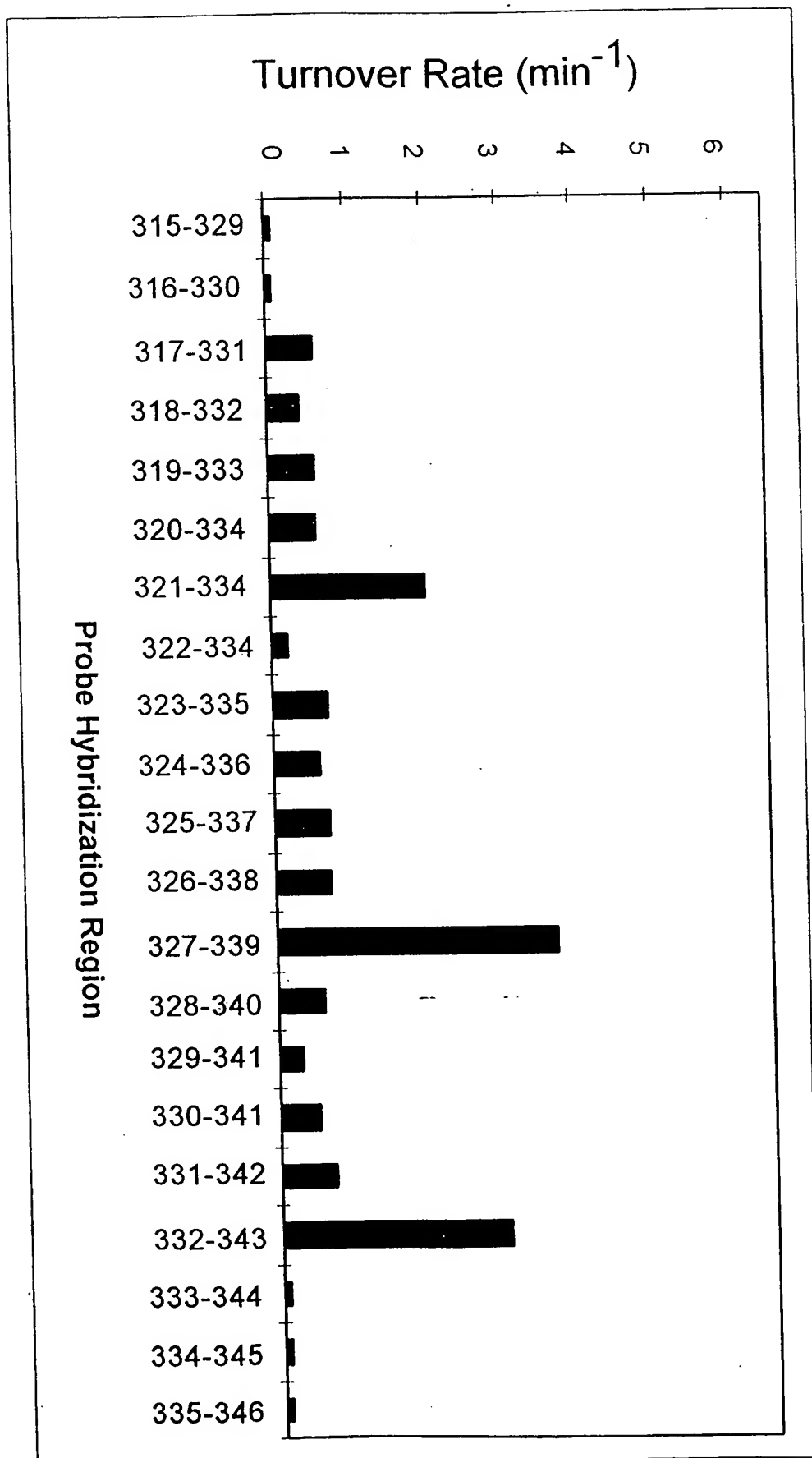


FIGURE 54A

FIGURE 54B



## FIGURE 55A

SEQ ID NO:158

### Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

### Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

### Primer 3

810 UCAGUAUUAA GCGGGGGAGA AUUAGAUCGA UGGGAAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUUAAA ACAUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUAGAA

960 GGCUGUAGAC AAUACUGGG ACAGCUACAA CCAUCCCUUC AGACAGGAUC

### Primer 4

1010 AGAAGAACUU AGAUCAUUAU AUAAUACAGU AGCAACCCUC UAUUGUGUGC

1060 AUCAAAGGAU AGAGAUAAAA GACAC**CAAGG** AAGCUUUAGA CAAGAUAG**AG**

## FIGURE 55B

1110 **GAAGAGCAAA** ACAAAAGUAA GAAAAAAGCA CAGCAAGCAG CAGCUGACAC

1160 **AGGACACAGC** AAUCAGGUCA GCCAAAUAU CCCUAUAGUG CAGAACAUCC

Primer 5

1210 **AGGGGC**AAU GGUACAUCAG GCCAUAUCAC CUAGACUUU AAAUGCAUGG

1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGUU

1310 UUCAGCAUUA UCAGA**AGGAG** **Cc**ACCCACACA AGAUUUAAAC ACCAUGC~~UAA~~

1360 ACACAGUGGG GGGACAUC**A** **GC**AGCCAUGC AAAUGU~~UAAA~~ AGAGACCAUC

Primer 6

1410 **AAUGAGGAAG** CUGCAGAAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC

1460 UAUUGC**ACCA** GGCCAGAUGA GAGA**ACCAAG** **GG**GAAGUGAC AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCCAGUAG GAGAAAUUUA UAAAAGAUGG AUAAUCCUGG GAUUA~~AAUAA~~

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAU AGACAAGGAC

1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA

1710 **GCCGAGCAAG** CUUC**ACAGGA** GGUAAAAAU **UGGA**UGACAG AAACCUUGUU

## FIGURE 55C

1760 GGUCCAAAAU GCGAACCCAG AUUGUAAGAC UAUUUUAAAA GCAUUGGGAC

Primer 8

1810 **CAGC**GGCUAC ACUAGAAGAA AUGAUGACAG CAUGUC**AGGG** AGU**AGG**AGGA

1860 CCCGGCCAUA AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

1910 UUCAGCUACC AUA AUGAUGC **AGAGAGG**CAA UUUUAGGAAC CAAAGAAAGA

1960 UUGUUAAGUG UUUCAAUUGU GGCAAAGA**AG** **GGCACACAGC** CAGAAAUUGC

2010 AGGGCCCCUA GGAAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

2060 AAUGAAAGAU UGUACUGAGA G



FIGURE 56

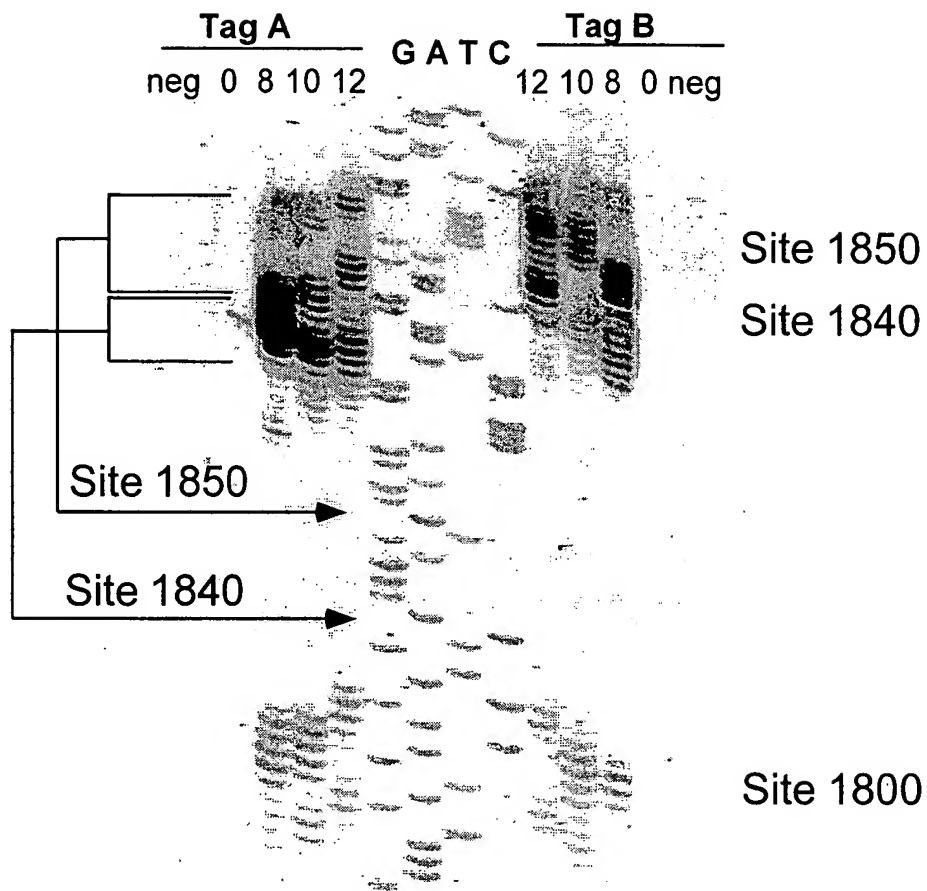


FIGURE 57

(SEQ ID NO:188)	CGTATTCCGGTCTCAAAACCGACTTGCT-5'	13
(SEQ ID NO:187)	AGGTATTCCGGTCTCAAAACCGACT	12
(SEQ ID NO:186)	ACGGTATTCCGGTCTCAAAACCGAC	10=11
(SEQ ID NO:185)	CCCGGTATTCCGGTCTCAAAACCGA	9
(SEQ ID NO:184)	CGCCGGTATTCCGGTCTCAAAACCG	8
(SEQ ID NO:183)	CGGCCGGTATTCCGGTCTCAAAAC	7
(SEQ ID NO:182)	AGGCCGGTATTCCGGTCTCAAAAC	6
(SEQ ID NO:181)	ATGGCCGGTATTCCGGTCTCAAAA	5
(SEQ ID NO:180)	ACTGGCCGGTATTCCGGTCTCAAA	4
(SEQ ID NO:179)	ACCTGGCCGGTATTCCGGTCTCAA	3
(SEQ ID NO:178)	ATCCTGGCCGGTATTCCGGTCTCA	2
(SEQ ID NO:177)	ACTCCTGGCCGGTATTCCGGTCTC	1
5'-CAUGCAGGAGUAGGACCCGGCCAUAGGCAAGUUUGGCUGAAGCAAUGAG-3'	(SEQ ID NO:158)	
1 CAGTCCCTCATC	(SEQ ID NO:164)	
2 AGTCCCTCATCC	(SEQ ID NO:165)	
3 GTCCCTCATCCT	(SEQ ID NO:166)	
4 TCCCTCATCCTC	(SEQ ID NO:167)	
5 CCCTCATCCTCC	(SEQ ID NO:168)	
6 CCTCATCCTCCT	(SEQ ID NO:169)	
7 CTCATCCTCCTG	(SEQ ID NO:170)	
8 TCATCCTCCTGG	(SEQ ID NO:171)	
9 CATCCTCCTGGG	(SEQ ID NO:172)	
10 ATCCTCCTGGGC	(SEQ ID NO:173)	
11 TCCTCCTGGGC	(SEQ ID NO:174)	
12 CCTCCTGGGCC	(SEQ ID NO:175)	
13 CTCCTGGGCCGAAA-FL-5'	(SEQ ID NO:176)	

FIGURE 58

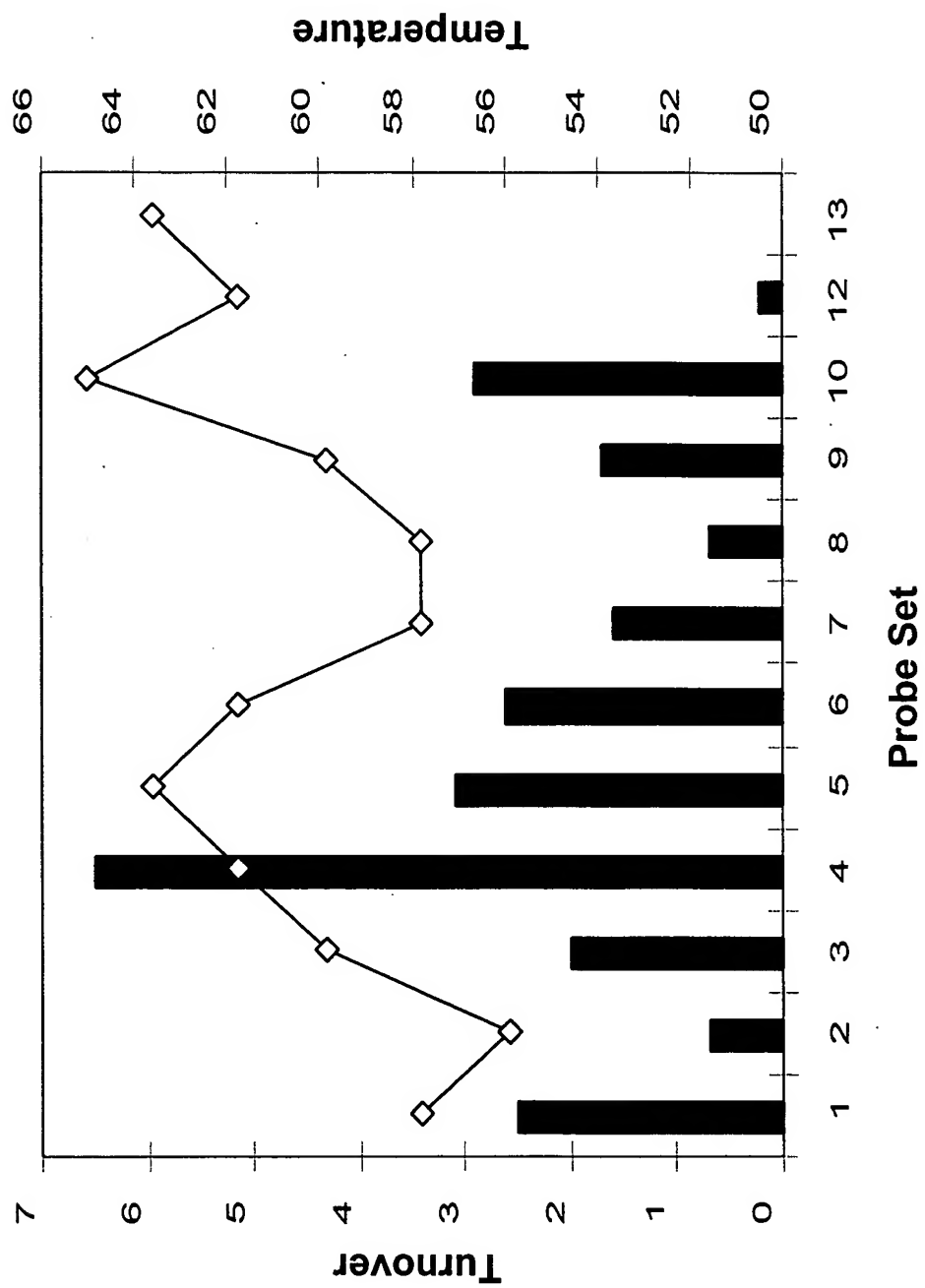


FIGURE 59

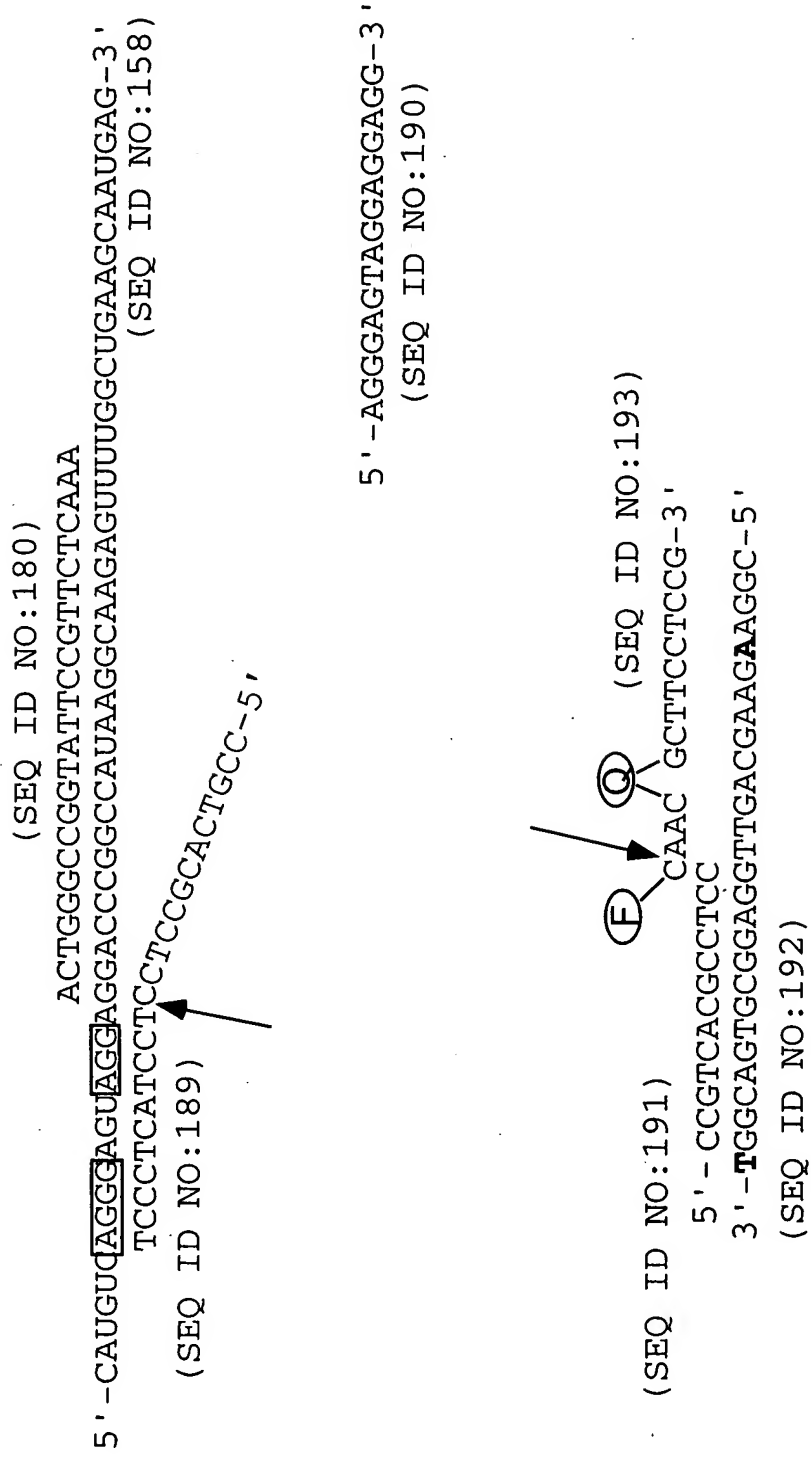
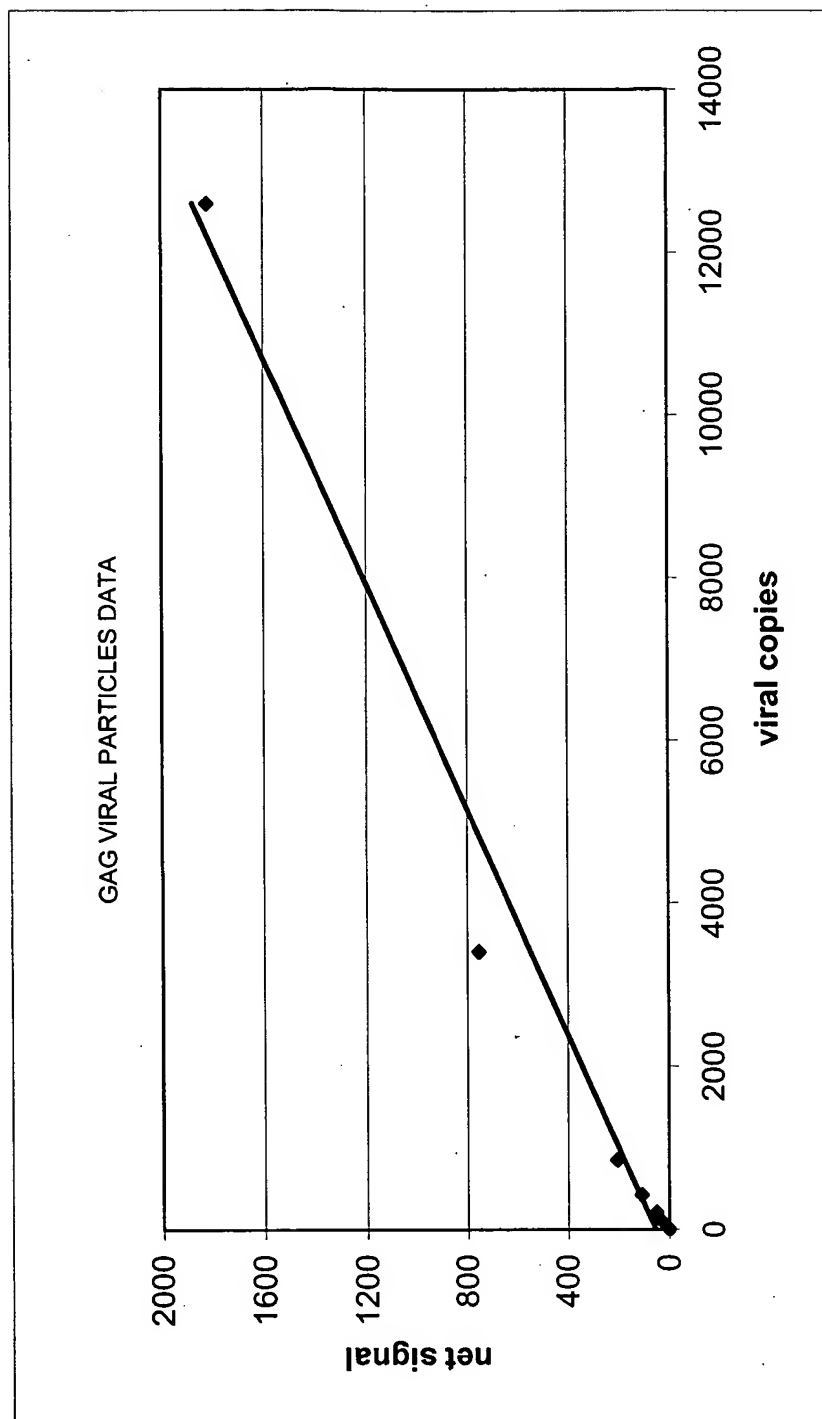


FIGURE 60



## FIGURE 61A

SEQ ID NO:159

primer 1  
3300 AGCUGGACUG UCAAUGACAU ACAGAA**GUUA** **GUGGGG**AAAU UG**AAUUGGGC**

3350 AAGUCAGAUU **UACCCAGGGA** UUA**AAAGUAAG** GCAAUUAUGU AAACUCCUUA

3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUAACAGA AGAAGCAGAG

3450 CUAGAA**CUGG** CAGAAAACAG AGAGAUUCUA AAAGAACCAG UACAUGGAGU

primer 2  
3500 GUAUUAUGAC **CCAUCAAAAG** ACUUAUAGC AGAAAU**ACAG** **AAGCAGGGGC**

3550 **AAGGCCAAUG** GACAUAUCAA AUUUUA**CAAG** AGCCAUUUAA AAAUCUGAAA

3600 ACAGGAAAAU AUGCAAGAAU **GAGGGG**UGCC CACACUAAUG AUGUAAAACA

3650 AUUAACAG**GAG** **GCAGUG**CAAA AAUAACCAC AGAAAGCAUA GUAAUAUGGG

primer 3  
3700 GAAAGACUCC UAAAUUUAAA **CUG**CCCAUAC AAAAGGAAAC AUGGGAAACA

3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU

3800 UAAUACCCCU CCCUAGUGA AAUUA**UGGUA** CCAGUUAGAG AAAGAACCCA

3850 UAGU**AGGAGC** AGAAACCUUC UAUGUAGAUG **GGGCAGCUAA** **CAGGGAGACU**

primer 4  
3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU **AGAGGAAGAC** AAAAAGUUGU

## FIGURE 61B

3950 CACCCUAACU GACACAACAA AUCAGAAGAC UGAGUUACAA GCAAUUUAUC  
4000 UAGCUUUGCA GGAUU**CGGGA** UUAGAAGUAA ACAUAGUAAAC AGACUCACAA  
4050 UAUGCAUUAG GAAUCAUUCA **AGCACAACCA** GAUCAAAGUG AAUCAGAGUU  
primer 5  
4100 AGUCAAUCAA AUAUA**GAGC** AGUUAUUAAA AAAGGAAAAG GUCUAUC**UGG**  
4150 **CAUGGGUACC** AGCACACAAA GGA**AUUGGAG** GAAUGAACA AGUAGAUAAA  
4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGAU**UAA**  
4250 **GGCCCAAGAU** GAACAUGAGA AAUAUCACAG UAAU**UGGAGA** GCAAUGGCUA  
primer 6  
4300 GUGAUUUUAA CCUGCCACCU GUAGUAGCAA AAGAAU**AGU** **AGCCAGCUGU**  
4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG  
4400 UCCAGGAAUA UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUAUCC  
4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUUAU U**GAAGCAGA** AGUUUUUCCA  
primer 7  
4500 GC**AGAAACAG** **GGCAGGAAAC** AGCAUUAUUU CUUUUAAAAU **UAGCAGGAAG**  
4550 **AUGGCCAGUA** AAAACAAUAC AU**ACUGACAA** **UGGCAGCAAU** UUC**ACCGGUG**  
4600 CUACGGUUAG GGCCGCCUGU UGGUGGGCGG GAAUCA**AGCA** **GGAAUUUGGA**

## FIGURE 61C

4650 AUUCCCUACA AUCCCCAAAG UCA**AAGG**AGUA GUAGAAUCUA UGAAUAAAGA

primer 8

4700 AUUAAAGAAA AUUAUAG**GAC** **AGG**UAAGAGA **UCAGGC**UGAA CAUCUUAAGA

4750 CAGCAGUACA AAUGGCAGUA UUCAUCCACA AUUUUAAAAG AAA**AGGGGGG**

4800 AUUGGGGGGU AC**AGUGCAGG** **GGAA**AGAAUA GUAGACAUAA UAGCAACAGA

4850 CAUACAAACU AAAGAAUUAC AAAAACAAAU UACAAAAAUU CAAAAUUUUC

primer 9

4900 GGGUUUUAUA CAG**GGAC**AGC AGAAAUCCAC UUUGGA**AAGG** ACCAGCAAAG

4950 CUCCUCUGGA AAGGUG**AAGG** GGCAGUAGUA AUACAAGAU AUAGUGACAU

5000 AAAA**GUAGUG** CCAAGAAGAA AAGCAAAGAU CAUUAGGGAU UAUGGAAAAC

5050 AGAUGGCAGG UGAUGAUUGU G



FIGURE 62

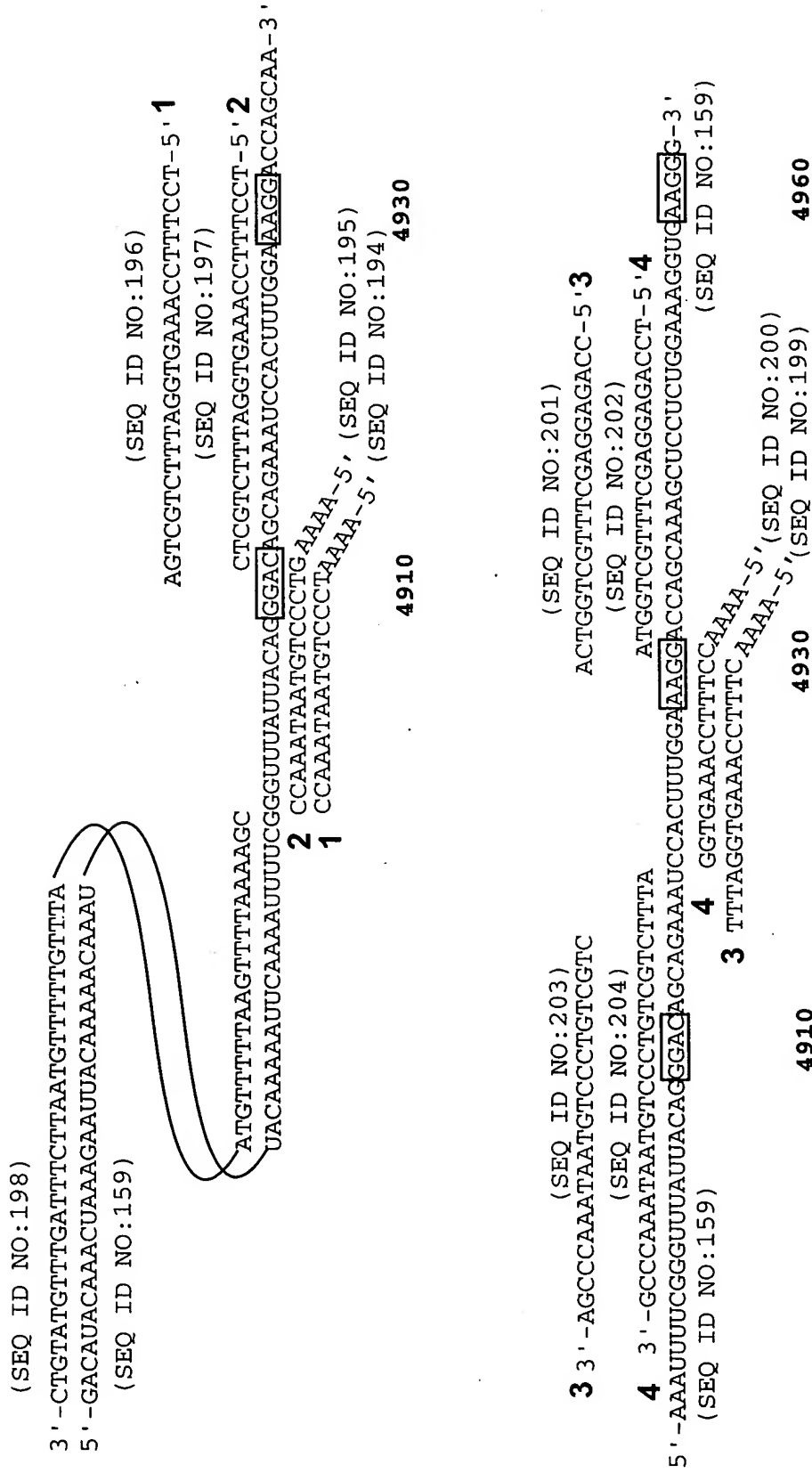


FIGURE 63

5 3' -TCCTGGTCGTTTCGAGGAGA (SEQ ID NO:213)  
 6 3' -CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:214)  
 5' -GAAAGGACCAGCAAAGCUCUCUGGAAAGGUGAAGGCGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUAGC-3'  
 4930  
 6 CTTTCCACTTCCA AAA-5', (SEQ ID NO:206)  
 5 CTTTCCACTTCA AAA-5', (SEQ ID NO:205)  
 4960  
 (SEQ ID NO:209)  
 ACCCGTCATCATTTATGTTCTATTATCATCATGTATTT-5' 5  
 (SEQ ID NO:210)  
 ACCGTCATCATTTATGTTCTATTATCATCATGTATTTTC-5' 6  
 (SEQ ID NO:159) 5000  
 7 3' -TCGAGGAGACCTTTCCAC (SEQ ID NO:215)  
 8 3' -TCGAGGAGACCTTTCCACT (SEQ ID NO:216)  
 5' -GAAAGGACCAGCAAAGCUCUCUGGAAAGGUGAAGGCGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUAGC-3'  
 4930  
 8 TCCCGTCATA AAA-5', (SEQ ID NO:208)  
 7 TTCCCGTCATA AAA-5', (SEQ ID NO:207)  
 4960  
 (SEQ ID NO:211)  
 CTCATTATGTTCTATTATCATCATGTATTTTCATCACGG-5' 7  
 (SEQ ID NO:212)  
 ACATTATGTTCTATTATCATCATGTATTTTCATCACGG-5' 8  
 (SEQ ID NO:159) 5000

1 4790 (SEQ ID NO:224) 4810 (SEQ ID NO:221)  
3'-TCCCCCCTAACCCCCCATG ATTTCTTATCATCTGTATTATCGTTGTCTGTATGT-5'  
5'-AAGAAAGGGGGGAAGUGCAGGGGAAGAGAAUAGUAGACAUAAUAGCAACAGACAUACAAACU-3'  
TCACGTCCCCAAA-5', (SEQ ID NO:159)

2,4 4790 (SEQ ID NO:225) 4810 (SEQ ID NO:222)  
3'-CTGTCGTATGTTTACCGTCATAAGTAGGT ACCCTAACCCCCCATGTCTAC-5'  
5'-AGACAGCAGUACAAAUAGGCAGUAUUAUCCACAAUUUAAAAGAAAGGGGGGAUUGGGGGUACAGUGCAGGGGAAG-3'  
GTTAAAAATTTTCTTTTCCCTATATA-5', (SEQ ID NO:159)  
GTTAAAAATTTTCTTTTCCCAAAA-5', (SEQ ID NO:220)  
GTTAAAAATTTTCTTTTCCCAAAA-5', (SEQ ID NO:218)

3 4790 (SEQ ID NO:222) 4810 (SEQ ID NO:223)  
ACCCCTAACCCCCCATGTCTAC-5' CATCATCTGTATTATCGTTGTCTGTATGTTGATTC  
5'-AAAGGGGGGAAGUGCAGGGGAAGAGAAUAGUAGACAUAAUAGCAACAGACAUACAAACUAAAGAA-3'  
GTECCCTTTCTTAAA-5', (SEQ ID NO:159)  
GTTAAAAATTTTCTTTTCCCAAAA-5', (SEQ ID NO:219)

FIGURE 65

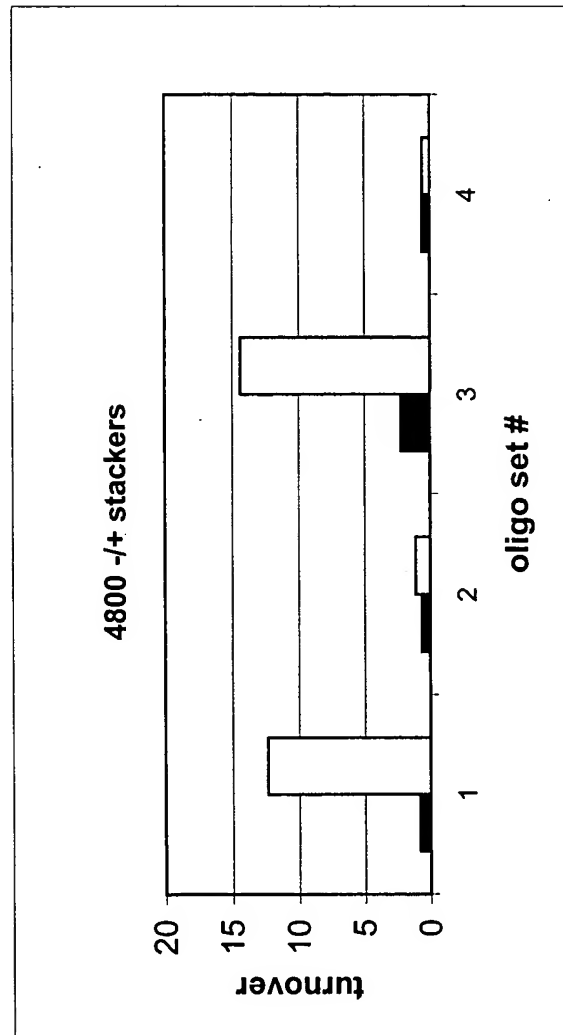


FIGURE 66

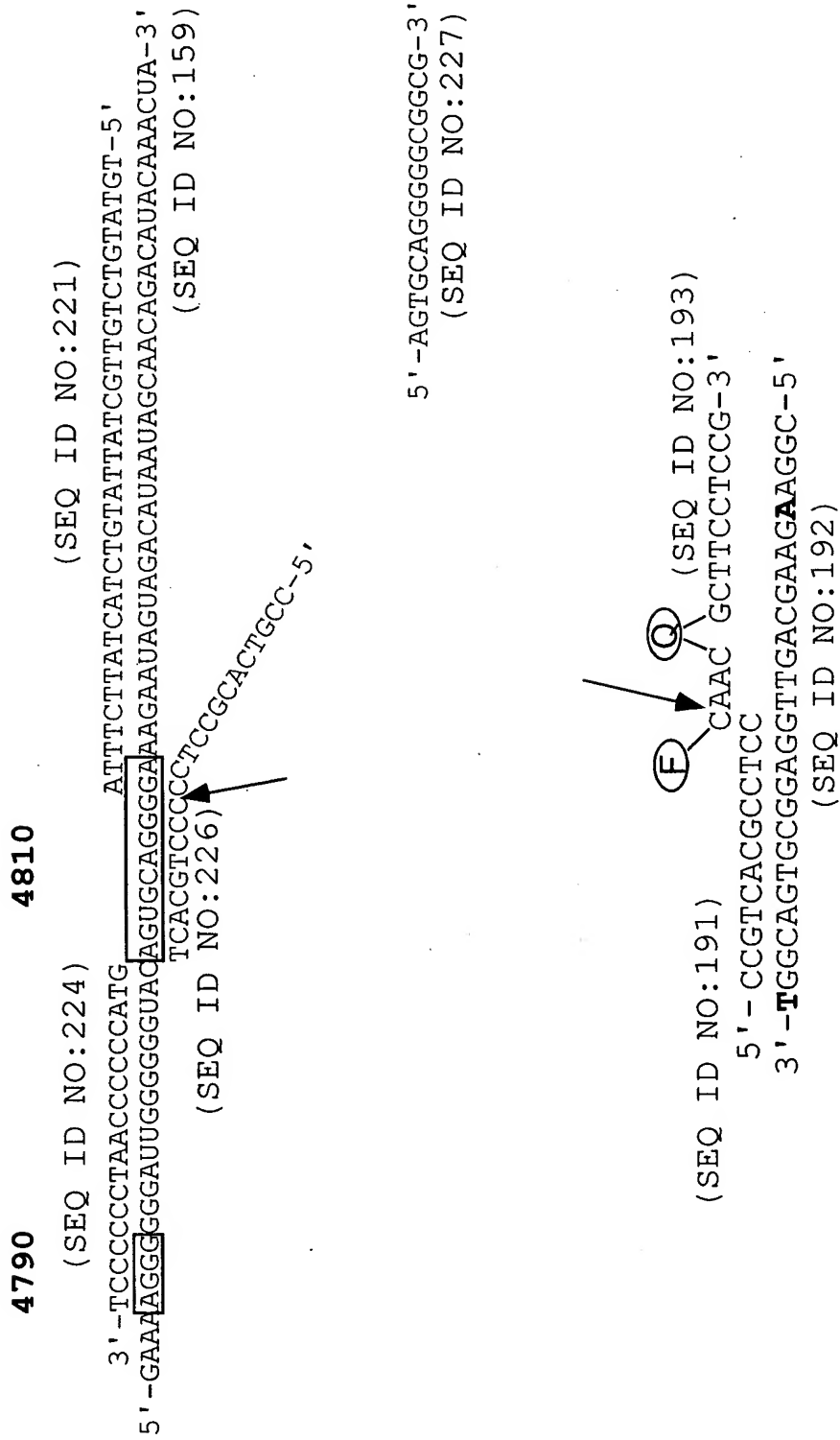


FIGURE 67

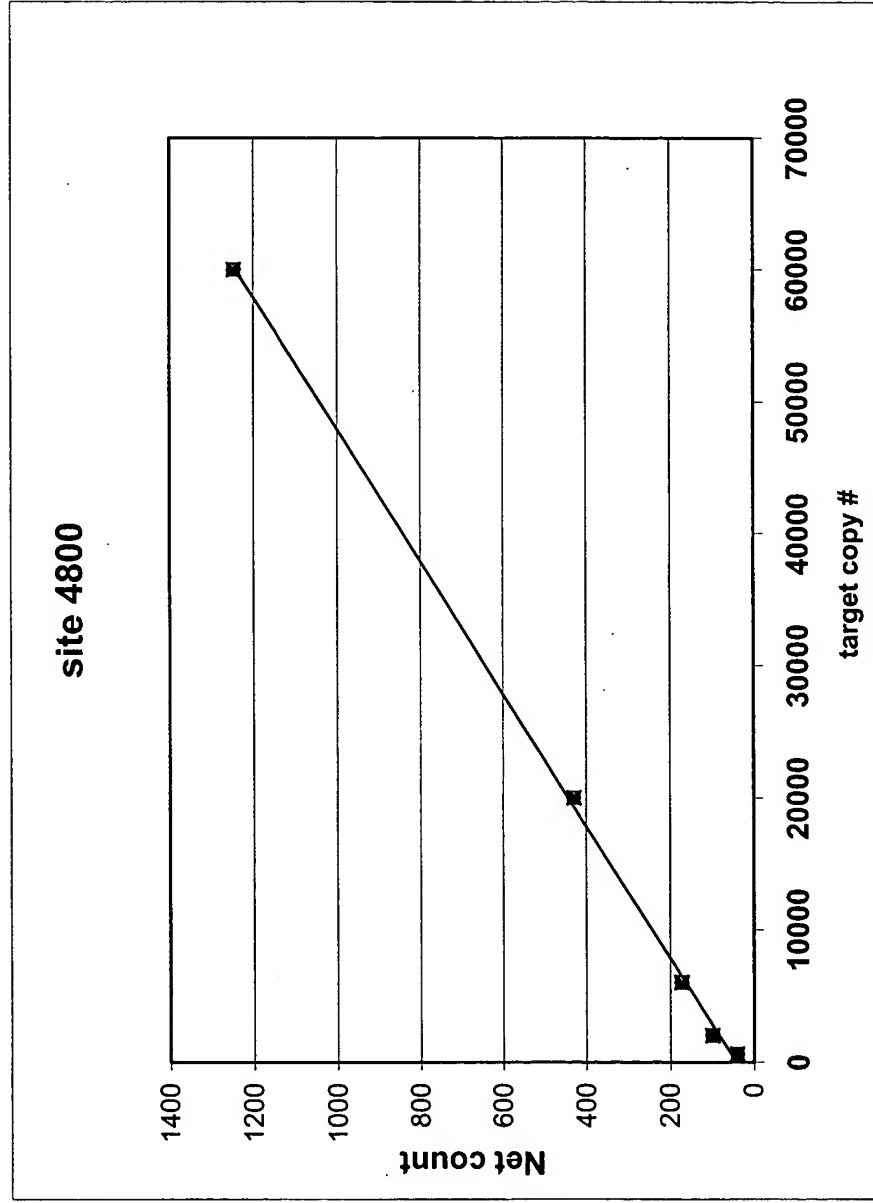


FIGURE 68

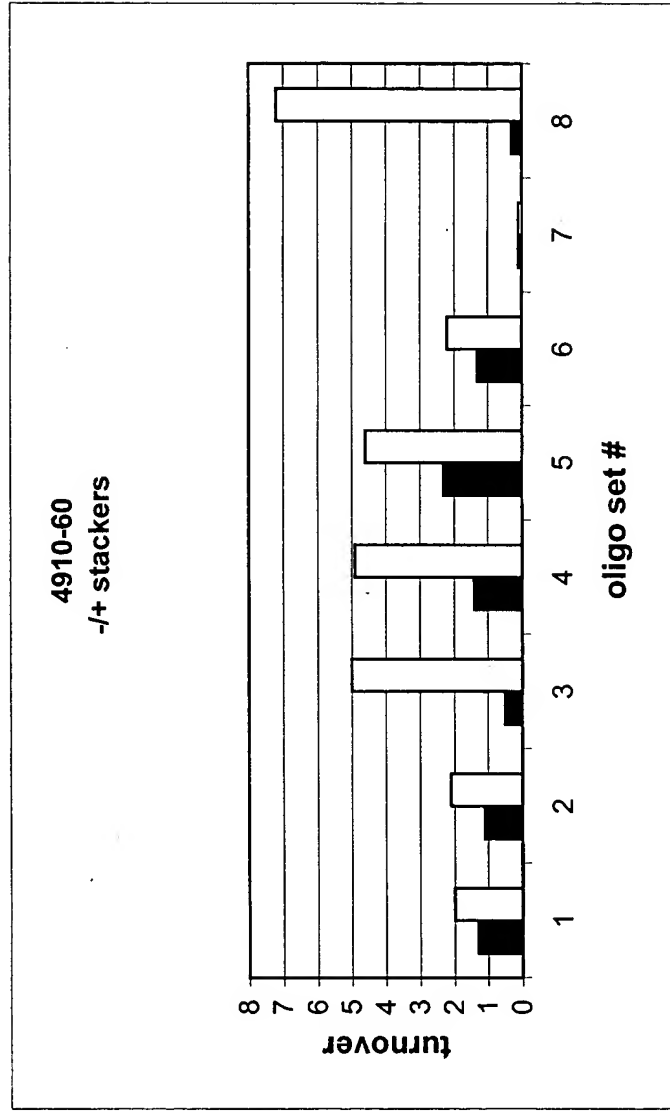


FIGURE 69

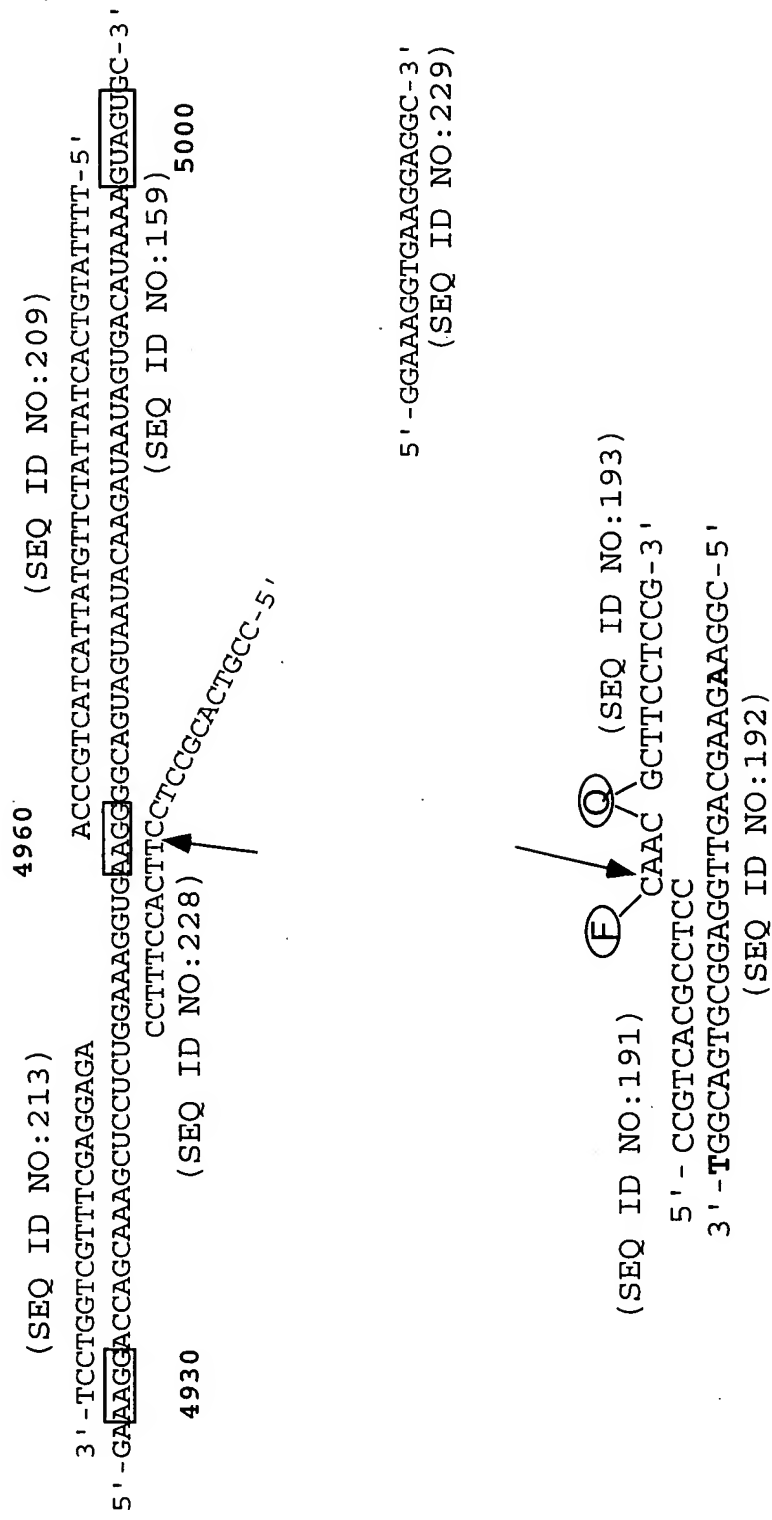
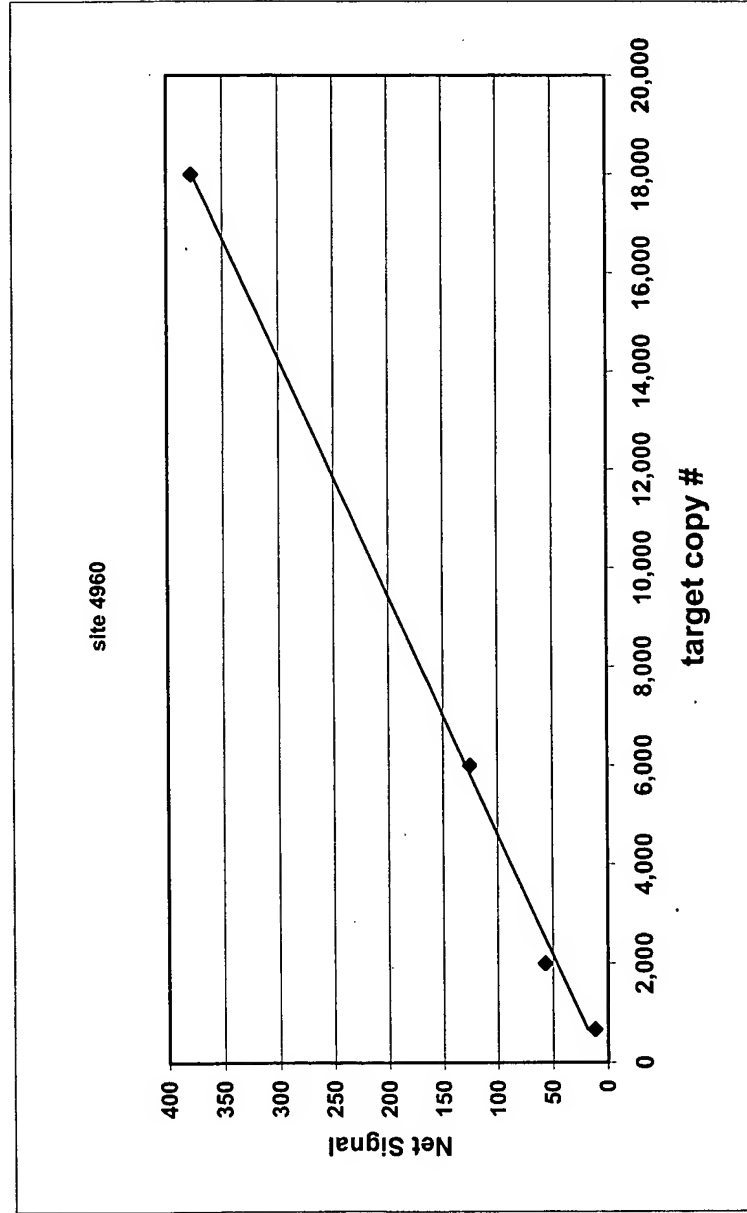




FIGURE 70



## FIGURE 71

### Human PSP94

383-31-1 5'-TET-CCTGCTTATCACAATGAA-3' (SEQ ID NO:230)

383-31-3 5'-TET-ACATGCACTTGCTACGAAAC-3' (SEQ ID NO:231)

SEQ ID NO:232

CCUGCUUAUCACAAUGAAUGUUCUCCUGGGCAGCGUUGUGAUCUUUGCCACCUUCGUGA  
CUUUAUGCAAUGCAUCAUGCUAUUUCAUACCUA AUGAGGGAGUUC CAGGAGAUUCAACCA  
GGAAAUGCAUGGAUCUCAAGGAAACAAACACCCAAUAAACUCGGAGUGGCAGACUGAC  
AACUGUGAGACAUGCACUUGCUCGAAACAGAAAUUUC AUGUUGCACCCUUGUUUCUAC  
ACCUGUGGGUUAUGACAAAGACACUGCCAAAGAAUCUUCAAGAAGGAGGACUGCAAGU  
AUAUCGUGGUGGAGAAGAAGGACCCAAAAAGACCUGUUCUGUCAGUGAAUGGAUAAUC  
UAAUGUGCUUCUAGUAGGCACAGGGCUCCCAGGCCAGGCCUCAUUCUCCUCUGGCCUCUA  
AUAGUCA AUGAUUGUGUAGCCAUGCCUAUCAGUAAAAAGAUUUUUG

## FIGURE 72

### Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)

520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAAUGCAGAUUUUCGUGAAAACCCUUA<sup>CGG</sup>GGAAGACCAUCACCCUCGAG  
GUUGAACCCUCGGAUACGAUAGAAAAUGUA<sup>AAGGC</sup>CAAGAUCCAGGAUAAGGAAGGAAU  
UCCUCCUGACAGCAGAGACUGAUCUUUGCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG  
UCUGACUACAAUAUUCAAAAGGAGUCUACUCUUCAUCUUGUGUUGAGACUU<sup>CGUGGUG</sup>G  
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCCAAGAAGAAUAAGCACAAGAGAAA  
GAAGGUUAA<sup>GCU</sup>GGCUGUCCUGAAAUAUUUAUAAGGUGGAUGAGAAUGGC AAAAUUAGUC  
GCCUUCGUCGAGAGUGCCCUUCUGAUGAAUGUGGUGCUGGGGUGUUUAUGGCAAGUCACU  
UUGACAGACAUUAUUGUGGCAAAUGUUGUCUGA

## FIGURE 73

### HCV-1a 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)  
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)  
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)  
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU  
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUCCCGGGAGAG  
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC  
UUGGAUAAACCCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCGCAAGACUGCUAGCCG  
AGUAGUGUUGGUGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC  
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

## FIGURE 74

### HCV-1b 5'-UTR:

898-28-02 5'-TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)  
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)  
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)  
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

### SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU  
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUCCCGGGAGAG  
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAUUGCCAGGACGACCGGGUCCUUUC  
UUGGAUCAACCCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCCCGAGACUGCUAGCCG  
AGUAGUGUUGGUGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC  
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

## FIGURE 75

### HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)  
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)  
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)  
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

### SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU  
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGGCCCCCCCUC[CCG]GGAGAG  
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAUUGCCGGGAAGACUGGGUCCUUUC  
UUGGAUAAACCCACUCUAUGCCCGGCCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGA  
GUAGCGUUGGGUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC  
GGGAGGUCUCGUAGACCGU[GCACCAUGAG]

## FIGURE 76

### HCV 3a 5'-UTR:

898-28-03 5'-TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)  
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)  
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)  
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

### SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUCUGUCUUCACGCGGAAAGCGC  
CUAGCCAUGGCGUUAGUACGAGUGUCGUGCAGCCUCCAGGCCCCCCCCUC<sup>CCG</sup>GGAGAG  
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUCGCUGGGGUGACCGGGUCCUUC  
UUGGAA<sup>CAACCC</sup>GCUCAAUACCCAGAAAUUUGGGCGUG<sup>CCCC</sup>CGCGAGAUAC<sup>UAGCCG</sup>  
AGUAGUGU<sup>UGG</sup>GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC  
CCGGGAGGUCUCGUAGACCGU<sup>GCACCAUGAG</sup>

## FIGURE 77A

### Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5'-ACAAGGGAAGAGAGATGAGGAACCAG-3'	(SEQ ID NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ ID NO:247)
937-03-01	5'-TET- aagggaagagagatgag-3'	(SEQ ID NO:248)
937-03-02	5'-TET-aggagtttgcaagaaac-3'	(SEQ ID NO:249)
937-03-03	5'-TET-ggtgctgtcctgg-3'	(SEQ ID NO:250)
937-03-04	5'-TET-cagttttggatctttgatg-3'	(SEQ ID NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ ID NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ ID NO:253)
937-03-07	5'-TET-caatactgcagatggag-3'	(SEQ ID NO:254)
937-03-08	5'-TET-aagccaggtattgca-3'	(SEQ ID NO:255)
937-03-09	5'-TET-ctattgtttctgcacaga-3'	(SEQ ID NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ ID NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ ID NO:258)



## FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAAUCAUAUCCAGGA  
GUUUGCAAGAAACAGGUGCUUAAACACUAAUUCACCUCCUGAACCAAGAAAUAUGGGCUGU  
GACCGGAAUCUGUGGGCUCaucgCUGGGGCUGUCAUUGGUGCUGUCCUGGCUGUGUUUGG  
AGGUAAUUCUAAUGCCAGUUUGGAGACCUGCUUUAUCCAAGACAAUUAAGCAAGUUG  
UCCUCGAAGAAGGUACAAUUGCUUUUAAAAUUGGGUUAAAAACAGGCACAGAAGUUUAC  
AGACAGUUUUGGAUCUUUGAUGUGCAAAAUCCACAGGAAGUGAUGAUGAACAGCAGCAA  
CAUUCAAGUUAAGCAAAGAGGUCCUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA  
AUGUAACCCAGGACGCUGAGGACAACACAGUCUCUUUCCUGCAGCCCAAUGGUGCCAUUC  
UUCCGAACCUUCACUAUCAGUUGGAAACAGAGGCUGACAACUUCACAGUUCUCAAUCUGGC  
UGUGGCAGCUGCAUCCCAUAUCUAUCAAUAUCAAUUUGUCAAUGAUCCUCAAUUCAC  
UUUAUACAAGUCAAAAUCUUCUAUGUCCAAGUCAGAACUUUGAGAGAACUGUUUUGG  
GGCUAUAGGGAUCCAUUUUUGAGUUUGGUUCCGUACCCUGUUACUACUACAGUUGGUCUG  
UUUUAUCCUUAACAACAUAACUGCAGAUGGAGUUUAUAAAGUUUUCAAUGGAAAAGAUAA  
CAUAAGUAAAGUUGCCAUAAUCGACACAUUAAGGUAAAAGGAUUCUGUCCUAUUGGG  
AAAGUCACUGCGACAUGAUUAAUGGUACAGAUCCAGCCUCAUUUCCACCUUUUGUUGAG  
AAAAGCCAAGUAUUGCAGUUCUUUUCUUCUGAUAUUUGCAGGUCAAUCUAUGCUGUAUU  
UGAAUCCGACGUUAAUCUGAAAGGAAUCCUGUGUAUAGAUUCGUUCUCCAUCCAAGG  
CCUUUGCCUCUCCAGUUGAAAACCCAAGACAACUAUUGUUUCUGCACAGAAAAAUUAUC  
UCAAAAAAUUGUACAUCAUAUGGUGUGCUAGACAUCAGCAAUGCAAAGAAGGGAGACC  
UGUGUACAUAUUCACUUCUCAAUUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA  
UGGAUUAACCCAAAUGAAGAAGAACAUAGGACAUAUUGGAUAUUAACCUAUAAUCUG  
GAUUCACUUUAACAUUUGCAAACGGCUGCAGGUCAACCUAUUGGUCAAGCAUCAGAA  
AAAAUUCAAGUAUUAAGAAUCUGAAGAGGAACUAUAUUGUGCCUAUUCUUUGGCUAA  
UGAGACUGGGACCAUUGGUGAUGAGAAGGCAA

## FIGURE 78

### Human Ribosomal Protein L5 mRNA

761-47-01	5'-ATGGGGTTTGTAAAGTTG-3'	(SEQ ID NO:260)
761-47-02	5'-GCTGGGTTTAGCTCTCAGCAGCCCGC-3'	(SEQ ID NO:261)
937-05-01	5'-TET- atggggtttgttaaagtt-3'	(SEQ ID NO:262)
937-05-02	5'-TET- gaagacgacgagagg-3'	(SEQ ID NO:263)
937-05-03	5'-TET- ggatgatagttcgtgtg-3'	(SEQ ID NO:264)
937-05-04	5'-TET- gctgcagcatattgta-3'	(SEQ ID NO:265)
937-05-05	5'-TET- ctgctatttgatgca-3'	(SEQ ID NO:266)
937-05-06	5'-TET- gcagaagtacatcgga-3'	(SEQ ID NO:267)
937-05-07	5'-TET- gacatgatggaggaga-3'	(SEQ ID NO:268)
937-05-08	5'-TET- agaagaaggatcggg-3'	(SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUUGUUAAGUUGUUAAGAAUAAGGC CUACUUUAAGAGAUACCAAGUGAAAUU  
 UAGAAGACGACGAGAGGGUAAAACUGAUUAUUAUGCUCGGAAACGCUUGGUGAUACAAG  
 AUAAAAUAAUAC AACACACCC AAAUACAG GAUGAUAGUUCGUGUGACAAACAGAGAU  
 AUCAUUGUCAGAUUG CUUAUGCCC GUUAUAGAGGGGAUAUGAUAGUCUGCGCACGUUA  
 UGCACACGAACUGCCAAAUAUGGUGUGAAGG UUGGCCU GACAAUUAUGCUGCAGCAU  
 AUUGUACUGGCCUGCUGC UGGCC CGCAGGCUUCUCAAUAGGU UUGGCAUGG ACAAGAUC  
 UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAUGUGGAAAGCAUUGAUGGUCAG  
 CCAGGUGCCUUCACCUGCUAUU UGGAUGCAGGCC UUGCCAGAACUACCACUGGCAAUAA  
 AGUUUUUGGUGC CCUGAAGGGAGC UGUGGAUGGAG GCUUGUCUAUCCCUCACAGUACCA  
 AACGAUU CCCU GGUUAUGAUUCUGAAAGCAAGGAUUUAAUGCAGAAGUACAUC GGAAG  
 CACAUC AUGG GCCAGAAUGUUGCAGAUU ACAUGC GC UACUUAU UGGAAGAAGAUGAAGA  
 UGCUUACAAGAAACAGUUCUCUCAAUACAUAAGA ACAGC GUAACU CCAG ACAUGAUGG  
 AGGAGAUGUAUAAGAAAGCUCAUGCUGCUAUA CGA GAGAAU CCA GUCUAUGAA AAGAAG  
 CCCAA GAAAGAAGUUAAAAA GAAGAGGUGGAACCGUC CCAAAUGUCC CUU GCUCAGAA  
 GAAGGAUC GG GUAGCUCAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG  
 AGAGCUAAACCCAGC

## FIGURE 79A

### Mouse Scavenger Receptor Class B Type I mRNA Oligonucleotides

726-39-01	5'-GCTCAAGAATGTCCGCATAGACCCG-3'	(SEQ ID NO:271)
666-34-01	5'-CTGGTCCCTGAGTTGTTTTTGC-3'	(SEQ ID NO:272)
937-01-01	5'-TET- GCTCAAGAATGTCCG-3'	(SEQ ID NO:273)
937-01-02	5'-TET- gggatgtggaaggag-3'	(SEQ ID NO:274)
937-01-03	5'-TET- ggaccctatgtctacag-3'	(SEQ ID NO:275)
937-01-04	5'-TET- acatcttggtcctgg-3'	(SEQ ID NO:276)
937-01-05	5'-TET- tctcaacacgtacctc-3'	(SEQ ID NO:277)
937-01-06	5'-TET- cggactcagcaaga-3'	(SEQ ID NO:278)
937-01-07	5'-TET- caaggggtgtttgaagg-3'	(SEQ ID NO:279)
937-01-08	5'-TET- ctctgtttctctccca-3'	(SEQ ID NO:280)
937-01-09	5'-TET- gtgaagatgcagctg-3'	(SEQ ID NO:281)
937-01-10	5'-TET- agctggtgctgatg-3'	(SEQ ID NO:282)
937-01-11	5'-TET- caggcctactctgag-3'	(SEQ ID NO:283)
937-01-12	5'-TET- ggactctctcagcg-3'	(SEQ ID NO:284)

## FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCCGCAUAGA[CCC]GAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUCC  
CCGUCCC UUUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAAC[GAG]GUCCUC  
AACGGCCAGAAGCCAGUAGU[CCGG]GAGCGUGGACCCUAUGUCUAC[AGG]GAGUUCAGACA  
AAAGGUCAACAUCACCUUCAUGA[CAACGACACC]GUGUCCUUCGUGGAGAA[CCGCAGC]C  
UCCAUUUCCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUUGUACUGCCUAACA  
UCUUGGUCCUGGGGGGUCGAUAUUG[AUGGAG]AGCAAGCCUGUGAGCCUGAAGCUGAUG  
AUGACCUUGGCGCUGGUCACCAUGGGGCCAGCGUGCUUUUAUG[AACC]GCACAGUUGGUGA  
GAUCCUGUGGGGCUAUGACGAUCCCUUCGUGCAUUUUCUACAACACGUACCUC CAGACA  
GCUUCCCAUAAAGGGCAAUUUGGCCUGUUGUUGGGAUGAACACUCGAAUUC[UGG]GG  
UCUUCACUGUCUUC[ACGG]GCGUCCAGAAUUUC[AGCA]GGAUCCAUCUGGUGGACAAAUGG  
AACGGACUCAGCAAGAUCGAUUAU[UGGCAUUCAGAGCA]GUGUAACAUGAUCAA[UGG]GAC  
U[UCCGG]GCAGAUG[UGGGC]ACCCUUCA[UGACACC]CGA[AUCCUC]GCUGGAAUUCUUCAGCC  
[CGGA]GGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAUU  
CCCACGUAUCGCUUC[ACGGCC]CCCGAUACUCUGUUGCCAACGGGUCCGUCUACCCACC  
CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGUU  
UGGUGCGCCUCUGUUCUCUCCACCCCCACUUUUAAC[AACGCCGAC]CCUGUGUUGUCAG  
AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUUCUUGUUCUAGACAUCCA[U]  
[CCGGU]CACUGGGAUCCCCAUGAACUGUUCUGUGAAGAU[GCA]GC[UGA]GCCUCUACAUCAA  
AUCUGUCAAGGGCAUCGGGCAAACAGGGAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG  
GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCACGUUCUACACGCAGCUGGU  
GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGGCUUGGAGGCCUCCU  
GUUGCUGGUGCCCAUCAUCUGCCAACUGCGC[AGCCAGGA]GAAUGCUUUUUGUUUUGGA  
GUGGUAGUAAAAAGGGCUCCAGGAUAAGGAGGCCAUUCAGGCCUACUCUGAGUCCUGA  
UGUCACCAGCUGCCAAGGGCACGGUGCUGCAAGAAGCCAAGCUAUAGGGUCCUGAAGACA  
CUAUAAG[CCCC]CCAAACCUGAUAGCUUGGUCAGACCAGCCACCCAGUCCCUACACCCCCG  
CUUCUUGAGGACUCUCUCAGCGGACAGCCCACCAGUGCCAUGGCCUGAGCCCCCAGAUGU  
CACACCUGUCCGCACGCACGGCACAUGGAUGCCCACGCAUGUGCAAAAACAACUCAGGGA  
CCAG

## FIGURE 80A

### Rat CX3CR1 Accession No. U04808 Oligonucleotides

761-57-01	5'-taatacgactcactatagggacggaagtccaagagcatcactg-3'	(SEQ ID NO:286)
761-57-03	5'-gcaggtagctgggtccgta-3'	(SEQ ID NO:287)
781-65-01	5'-TET-ggaagtccaagagca-3'	(SEQ ID NO:288)
781-65-02	5'-TET-aatggcttctttggg-3'	(SEQ ID NO:289)
781-65-03	5'-TET-ggcgtcgccc-3'	(SEQ ID NO:290)
781-65-04	5'-TET-tacttccgcatcgtc-3'	(SEQ ID NO:291)
781-65-05	5'-TET-cttcttccctagttgtg-3'	(SEQ ID NO:292)
781-65-06	5'-TET-tgcctggccgt-3'	(SEQ ID NO:293)
781-65-07	5'-TET-gactctactaagaaccca-3'	(SEQ ID NO:294)
781-73-01	5'-TET-ccatcttagtggcgt-3'	(SEQ ID NO:295)
781-73-02	5'-TET-caacaagtgcctgg-3'	(SEQ ID NO:296)
781-85-01	5'-TET-aacacggcgtcac-3'	(SEQ ID NO:297)
781-85-02	5'-TET-tgattaccccgagg-3'	(SEQ ID NO:298)
781-85-03	5'-TET-acgctgttttcctg-3'	(SEQ ID NO:299)
781-85-04	5'-TET-tgagacacctgtacaa-3'	(SEQ ID NO:300)
781-85-05	5'-TET-gacggagacagtgg-3'	(SEQ ID NO:301)
781-85-06	5'-TET-caagcgagggagag-3'	(SEQ ID NO:302)

## FIGURE 80B

Rat CX3CR1 Accession No. U04808 (SEQ ID NO:303)

[illegible]

## FIGURE 81A

### Human Interleukin-1 beta (IL-1 $\beta$ ) Oligonucleotides

720-82-01 5'-  
gtaatttaatacgaactcactatagggaaggtgcagttttgcccaaggagtgctaaag-3'  
(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatttatctaataaaacatcat-3'  
(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3' (SEQ ID NO:306)  
781-50-02 5'-TET-gagagtggaccacac-3' (SEQ ID NO:307)  
781-50-03 5'-TET-gaatcagtgaagatgcc-3' (SEQ ID NO:308)  
781-50-04 5'-TET-cattgtaccatgaaatatcc-3' (SEQ ID NO:309)  
781-50-05 5'-TET-gaactttaatttcaggaattg-3' (SEQ ID NO:310)  
781-50-06 5'-TET-ccctagtctgctagc-3' (SEQ ID NO:311)  
781-50-07 5'-TET-ttcaagtgtacttattaacc-3' (SEQ ID NO:312)  
781-72-01 5'-TET-aagctggccgtg-3' (SEQ ID NO:313)  
781-72-02 5'-TET-tgcagttttgcccaag-3' (SEQ ID NO:314)

## FIGURE 81B

Human Interleukin-1 beta (IL-1 $\beta$ ) (GenBank Accession #  
M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAGUGAAUGAUGGCUUAUUA CAGUGGCAAUGAGGAUG  
ACUUGUUCUUUGAAGCUGAUGGC CCUAAACAGAUGAAGUGCUCCUUC CAGGACCUGGAC  
CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAAUCU CCGACCAC CACUA CAGCAAGG  
CUUCAGGCAGGCCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUU C  
CCUGCC CACAGACCUUCCAGGAGAAUGA CCUG AGCACCUCUUCUCCCUUCAUCUUUGAA  
GAAGAACCUAUCUUCUUCG ACACAUGG GAU AACGA GGCUUAUGUG CACGA UGCACCUGU  
ACGAUC ACUGAACUGCACGCUCCG GGACUCACAGCAAAAAGCUUGGUGAUGUCUGGUC  
CAUAUGAACUGAAAGCU CUCC ACCUC CAG GGGACAGGAUAUGGAGCAACAAGUGGUGUUC  
UCCAUGUCCUUUGUACAAGGAGAAGAAAGUAAUGACAAAUACCUGUGGCCUUGGGCCUC  
AAGGAAAAGAAUCUGUAC CUGUCCUGCG UGUUGAAAGAUGAUAAAGCCCACUCUACAGCU  
GGAGAGUGUAGAUC CCAAAAUUACCCAAAGAAGAUGGAAAAGCGAUUUGUCUUCAA  
CAAGAUAGAAAUCAAU AACAAAGCU GGAAUUGAG UCUG CCCAGUCCCCAACUGGUAC A  
UCAGCACCC UCUC AAGCAGAAAA CAUGC CCGUCUUC CUGGGAGGGACCAAAG GCGG CCG  
GAUAUAACUGACUUC ACCA UGCAAUUUGUGUCUUC CUAAAGAGAGCUGUACCCAGAGAG  
UCCUGUGCUGAAUGUGGACUCAAUCC CUAGGGCU GGCAGAAAGGGAACAGAAAGGUUUU  
UGAGUACGGCUAUAGCCUGGACUUUCCUGUUGUCUACACCAAUGCCCAACUGCCUGCCUU  
AGGGUAGUGCUAAGAGGAUCUCCUGUCCA UCAGCCA GGACAGUCAGCUCUCUCCUUU CA  
GGGCCAAUCC CCAGC CCUUUUGUU GAGCCAGGCCUCUCUCAC CUCUCCUACUCACUU AA  
AGCCCGCC UGACAGA AACACGG CCACAUUUGGUUCUAAGAAACCUCUGUCAUUCGCU  
CCCACAUUCUGAU GAGCAACCGCU UCCCUAUUUUAUUUAUUUAUUUGUUUGUUUUUA  
UUCAUUGGUCUAAUUUAUU CAAAGGGGGC AAGAAGUAGCAGUGUCUGUAAAAGAGCCUA  
GUUUUUAUAGCUAUGGAAUCAAUUCAAUUUGGA CUG GUGUGCUCUCUUUAAAUCAAGU  
CCUUUAA UUAAGAC UGAAAUAU AUAAGCU CAGAUUAUUU AAAUG GGAUAUUUAUAA A  
UGAGCAAAUAUCAUACUGUUA



## FIGURE 82A

### Human Interferon gamma Oligonucleotides

448-59-01	5'-TET-GCATCGTTTTGGGTTCTCTT	(SEQ ID NO:316)
448-59-02	5'-TET-ACTTTAAAGATGACCAGAGC	(SEQ ID NO:317)
448-79-01	CACATTGTTCTGATCATCTG	(SEQ ID NO:318)
448-79-02	CGGTAAGTGAATGTC	(SEQ ID NO:319)
448-79-03	TAGTAAGTATATCAC	(SEQ ID NO:320)
448-79-04	GACATTCAAGTCAGTTACCG	(SEQ ID NO:321)
498-20-01	AATTTAATACGACTCACTATACACATTGTTCTGATCATCTG	(SEQ ID NO:322)
498-20-02	AATTTAATACGACTCACTATACGGTAAGTGAATGTC	(SEQ ID NO:323)
498-20-03	5'-TET-CACATTGTTCTGATCATCTG	(SEQ ID NO:324)
498-20-04	5'-TET-CGGTAAGTGAATGTC	(SEQ ID NO:325)
498-40-01	5'- AGTAATTTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA	(SEQ ID NO:326)
498-40-02	5'- AGTAATTTACGACTCACTATAGGGACGGTAAGTGAATGTCCAAC	(SEQ ID NO:327)
498-84-01	5'-TET-CATTCAGATGTAGCG	(SEQ ID NO:328)
498-84-02	5'-TET-GACTCATCAATCAAA	(SEQ ID NO:329)
498-84-03	5'-TET-GATTACAAGGCTTTA	(SEQ ID NO:330)

## FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCaucUGAAGAUCAGCUAUUAGAAGAGAAAGAUcAGUUAAGUCCUUU  
GGACCUGAUCAGCUUGAUACAAGAACUACUGAUUUCAACUUCUUUGGCUUAAUUCUCUC  
GGAAACGAUGAAAUAUACAAGUUUAUcUUGGCUUUUCAGCUCUGCAUCGUUUUGGGUUC  
UCUUGGCUGUACUGCCAGGACCCAUUGUACAAGAAGCAGAAAACCUUAAGAAAUAUU  
UUAAUGCAGGUCAUUCAGAUGUAGCGGAUAAUGGAACUCUUUUCUUAAGGCAUUUUGAAG  
AAUUGGAAAGAGGAGAGUGACAGAAAAUAUUGCAGAGCCAAAUUGUCUCCUUUUACUU  
CAAACUUUUUAAAAACUUUAAAGAUGACCAGAGCAUCCAAAAGAGUGUGGAGACCAUCA  
AGGAAGACAUGAAUGUCAAGUUUUUCAAUAGCAACAAAAGAAACGAGAUGACUUCGAAA  
AGCUGACUAAUUAUUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA  
UCCAAGUGAUGGCUGAACUGUCGCCAGCAGCUAAAACAGGGAAGCGAAAAAGGAGUCAG  
AUGCUGUUUCGAGGUCGAAGAGCAUCCCAGUAAUGGUUGUCCUGCCUACAAUAUUUGAAU  
UUUAAAUCUAAAUCUAUUUAUUAAUAUAACAUAUAUUUAUAUGGGGAUAUAUUUUUAGAC  
UCAUCAAUCAAUAAGUAUUUAUAAUAGCAACUUUUGUGUAAUGAAAAUGAAUAUCUAUU  
AAUAUAUGUAUAUUUAUAAUCCUAUAUCCUGUGACUGUCUCACUUAUCCUUUGUUUU  
CUGACUAAUUGGCAAGGCUAUGUGAUUACAAGGCUUUAUCUCAGGGGCCAACUAGGCA  
GCCAACCUAAGCAAGAUCCCAUGGGUUGUGUGUUUAUUUCACUUGAUGAUACAAUGAAC  
ACUUAUAAGUGAAGUGAUACUAUCCAGUUACUA

## FIGURE 83A

*Pneumocystis carinii* (NUCLEOTIDES 84-415 OF ACCESSION #  
AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGUGAUCUGGAAUAAAUUCAGAUUGC  
GACACUGUCAAAUUGCGGGGAAGCCCUAAAGAUUCAACUACUAAGCAGUUUGUGGAAAC  
ACAGCUGUGGCCGAGUUAUAGCCCUUGGUUAUAGUAACAAUGUUGAAUAUGAAUCUUUU  
GCGAGAUGAAUUGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG  
UUCAACGACUAGAUGGCAGUGGGUAUUGUAAGGAAUUGCAGUUUUCUUGCAGUGCUUAA  
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGUAUAU

*Candida albicans* (NUCLEOTIDES 72-418 OF ACCESSION #  
X74272) (SEQ ID NO:332)

GGGAGGCAAAAGUAGGGACGCCAUGGUUUCAGAAAUGGGCCGCGGUGUUUUUGACCUGC  
UAGUCGAUCUGGCCAGACGUAUCUGUGGGUGGCCAGCGGCGACAUAACCUGGUACGGGG  
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA  
UGGGGUUAAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCGUAGAG  
CAGCGAAAGGUAUGGGCUGGCUCUCUGAGUCGGCUUAAAGUACGUGCCGUCCCACACGA  
UGAAAAGUGUGCGGUGCAGAAUAGUUCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU  
UCUUGGAGCAAU

## FIGURE 83B

**Earwig R2 element** (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCUCUCAGCUGCUCACUUGCUGUUCUAAGUG  
AUAAUACCGUUGUUUUUUUAGUGGGUAUUCUUUUACGCUUUCGUAGGAGCGAGUCCCAC  
ACUCUUGGAGCAAUCCGGGGUAGUGCCUAAACGCAUUUCUUCAACGU

**Bombyx mori R2 element** (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAAGGGUGUAGAUCAGGCCCGUCUGUUUCUCCCCGGA  
GCUCGCUCCCUUGGCUUCCCUUAUAUAUUUUAACAUCAGAAACAGACAUUAAACAUCUA  
CUGAUCCAAUUUCGCCGGCGUACGGCCACGAUCGGGAGGGUGGGAAUCUCGGGGGUCUU  
CCGAUCCUAAUCCAUGAUGAUUACGACCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC  
GGCGAUG